

SEQUENCE LISTING

<110> Glaxo Group Limited

<120> Vaccine

<130> PG4961

<140> PCT/EP2003/011158

<141> 2003-10-01

<150> GB 0222953.2

<151> 2002-10-03

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1107

<212> DNA

<213> HPV

<400> 1

```
atggaagcta ttgccaagcg actggacgcc tgccaggagc agctgctgga gctgtacgag 60
gaaaacagca cagacctcca caagcacgtg ctgcactgga agtgcattgc ccacgagtca 120
gtgctcctgt acaaggccaa gcagatgggg ctgtcccaca tcgggatgca ggtcgtgccc 180
ccgctgaagg tgagcgaagc caagggccac aacgctatcg agatgcagat gcacctggag 240
agcctgctgc ggaccgaata cagcatggag ccctggactc tccaggagac gtcctacgaa 300
atgtggcaga ctctctccgaa gcgctgtttc gcaaagcgcg gcaagacagt tgagggtgaaa 360
ttcgatgggt gcgcaaacaa cacgatggac tacgtggtgt ggaccgatgt ctacgtgcag 420
gacaatgaca cctgggtgaa ggtacatagt atggtggatg ccaagggcat ctattacacc 480
tgcgggcagt tcaagacgta ctacgtcaac ttctgtcaagg aagccgaaaa gtatggttcc 540
accaagcact gggaggtgtg ttacgggagt actgtgatct gcagccccgc ctccgtgtcg 600
tccaccacc aggaagtgtg cattccggag agcaccacat acaccccggc ccaaacgagc 660
acgtctgtca gcagcagcac caaggaggac gccgtccaga cgcccccccg gaagagggcc 720
cggggggttc agcagtcttc ctgcaatgcc ctgtgcgttg ctcacatcgg ccctgtcgat 780
tctgggaacc acaatctcat cacgaacaac cagcaccagc accaaaggcg caacaactct 840
aacagctccg caactccaat agtgcagttc cagggggagt ccaactgcct caagtgtttc 900
cgctaccgcc tcaacgaccg ccaccgccac ctgttcgact tgatcagttc cacgtggcac 960
tgggccagca gcaaggcgcc ccacaaacac gctatcgtga cgggtgacct cgactccgag 1020
gagcagaggc agcagttcct ggacgtcgtg aagattcctc cgacaatcag ccacaagctt 1080
ggcttcatgt cctgcacact gctgtga 1107
```

<210> 2

<211> 368

<212> PRT

<213> HPV

<400> 2

```
Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Glu Gln Leu Leu
1          5          10          15
Glu Leu Tyr Glu Glu Asn Ser Thr Asp Leu His Lys His Val Leu His
20          25          30
Trp Lys Cys Met Arg His Glu Ser Val Leu Leu Tyr Lys Ala Lys Gln
```

35

40

45

Met	Gly	Leu	Ser	His	Ile	Gly	Met	Gln	Val	Val	Pro	Pro	Leu	Lys	Val
50						55					60				
Ser	Glu	Ala	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu
65					70					75					80
Ser	Leu	Leu	Arg	Thr	Glu	Tyr	Ser	Met	Glu	Pro	Trp	Thr	Leu	Gln	Glu
				85					90					95	
Thr	Ser	Tyr	Glu	Met	Trp	Gln	Thr	Pro	Lys	Arg	Cys	Phe	Ala	Lys	
			100					105					110		
Arg	Gly	Lys	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Ala	Asn	Asn	Thr
		115					120					125			
Met	Asp	Tyr	Val	Val	Trp	Thr	Asp	Val	Tyr	Val	Gln	Asp	Asn	Asp	Thr
	130					135					140				
Trp	Val	Lys	Val	His	Ser	Met	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr
145					150					155					160
Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Val	Lys	Glu	Ala	Glu
				165					170					175	
Lys	Tyr	Gly	Ser	Thr	Lys	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val
			180					185					190		
Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Thr	Gln	Glu	Val	Ser	Ile
		195					200					205			
Pro	Glu	Ser	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Ser	Thr	Leu	Val	Ser
		210				215					220				
Ser	Ser	Thr	Lys	Glu	Asp	Ala	Val	Gln	Thr	Pro	Pro	Arg	Lys	Arg	Ala
225					230					235					240
Arg	Gly	Val	Gln	Gln	Ser	Pro	Cys	Asn	Ala	Leu	Cys	Val	Ala	His	Ile
				245					250					255	
Gly	Pro	Val	Asp	Ser	Gly	Asn	His	Asn	Leu	Ile	Thr	Asn	Asn	His	Asp
			260					265					270		
Gln	His	Gln	Arg	Arg	Asn	Asn	Ser	Asn	Ser	Ser	Ala	Thr	Pro	Ile	Val
		275					280					285			
Gln	Phe	Gln	Gly	Glu	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu
		290				295					300				
Asn	Asp	Arg	His	Arg	His	Leu	Phe	Asp	Leu	Ile	Ser	Ser	Thr	Trp	His
305					310					315					320
Trp	Ala	Ser	Ser	Lys	Ala	Pro	His	Lys	His	Ala	Ile	Val	Thr	Val	Thr
				325					330					335	
Tyr	Asp	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile
			340					345					350		
Pro	Pro	Thr	Ile	Ser	His	Lys	Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu
		355					360					365			

&lt;210&gt; 3

&lt;211&gt; 1950

&lt;212&gt; DNA

&lt;213&gt; HPV

&lt;400&gt; 3

```

atggcagacg attccggtac tgagaacgaa ggttcttggtt gtaccggttg gttcatgggtt 60
gaagcaatcg ttcagcatcc gactgggtacc cagatctccg atgacgaaga cgaagaagtt 120
gaagattctg gttacgacat gggtgacttc atcgatgact ccaacatcac tcataactct 180
ctggaagcac aggctctggt taaccgccag gaagctgata cccattacgc tactgttcag 240
gacctgggag gcaaatatct gggtctctccg tacgtttccc cgatcaacac tatcgagaa 300
gcagttgagt ctgaaatctc cccgcgcctg gacgctatca aactgactcg tcagccgaag 360
aagggttaaac gtcgtctggt ccagactcgt gaactgaccg actccgggta cgggttatagc 420
gaagttgagg ctggcacccg caccaggtt gaaaaacacg gtgtaccgga aaacggcggc 480
gacggtcagg aaaaggacac cggccgcgac atcgagggtg aggaacacac cgaagctgaa 540

```

```

gctccgacta actctgttcg tgaacacgca ggtactgcgg gtatcctgga actgctgaaa 600
tgcaaagacc tgcgcgcggc tctgctgggc aaattcaaag aatgcttcgg cctgtctttc 660
attgacctga tccgtccgtt taagtctgac aaaactacct gtctggactg ggttgtagca 720
ggcttcggca tccaccactc tatctctgaa gcattccaga aactgatcga gccgctgtct 780
ctgtacgcgc acatccagtg gctgactaac gcttggggta tggttctgct ggtactgctg 840
cgctttaaag taaacaaatc tcgttccact gttgctcgta ctctggctac cctgctgaac 900
atcccggaga accagatgct gatcgaaccg ccgaaaatcc agtctggtgt agctgcactg 960
tactggtttc gtactggcat ctctaacgct agcactgtta tcggtgaagc accggaatgg 1020
atcactcgtc agaccgttat cgaacacggc ctggcagatt ctcagttcaa actgactgaa 1080
atgggttcagt gggcatacga caacgacatc tgcgaggaat ctgaaattgc gttcgaatac 1140
gctcagcgtg gcgacttcga ctccaacgct cgtgctttcc tgaacagcaa catgcaggct 1200
aaatacgtaa aagactgcgc taccatgtgc cgtcactaca aacacgcgga aatgcgtaaa 1260
atgtctatca aacagtggat caagcacgcg ggttctaaaa tcgaaggtag cggtactgg 1320
aaaccgatcg ttcagttcct gcgccatcag aacatcgaat tcatcccgtt cctgaccaa 1380
ttcaagctgt ggctgcacgg taccctgaaa aaaaactgca tcgctatcgt aggtccaccg 1440
gacactgaca agtcttactt ctgtatgtcc ctgatctctt tcctgggcgg cactgtaatc 1500
tctcacgtta actcttcttc ccatttctgg ctgcagccac tggtagacgc gaaagtagct 1560
ctgctggacg acgcgaccca gccgtgctgg atctacatgg atacttacat gcgcaacctg 1620
ctggacggta acccgatgtc tatcgaccgt aaacacaaag cgctgactct gatcaagtgc 1680
ccgccgctgc tggtaacttc taacatcgac atcaccaagg aagataaata caagtacctg 1740
cataccctgt ttactacctt tactttctcc aaccggttcc cgtttgatcg taacggtaac 1800
gctgttttac aactgtccaa cactaactgg aaatgcttct tcgagcgtct gtcttctctc 1860
ctggacatcc aggactctga agatgaagaa gatggttcta actctcaggc tttccgttgt 1920
gttccgggta ctgttggtcg tactctgtga 1950

```

<210> 4  
<211> 649  
<212> PRT  
<213> HPV

```

<400> 4
Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
 1          5          10          15
Trp Phe Met Val Glu Ala Ile Val Gln His Pro Thr Gly Thr Gln Ile
 20          25          30
Ser Asp Asp Glu Asp Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
 35          40          45
Asp Phe Ile Asp Asp Ser Asn Ile Thr His Asn Ser Leu Glu Ala Gln
 50          55          60
Ala Leu Phe Asn Arg Gln Glu Ala Asp Thr His Tyr Ala Thr Val Gln
 65          70          75          80
Asp Leu Gly Gly Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Asn
 85          90          95
Thr Ile Ala Glu Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
100          105          110
Ile Lys Leu Thr Arg Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Gln
115          120          125
Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
130          135          140
Gly Thr Gly Thr Gln Val Glu Lys His Gly Val Pro Glu Asn Gly Gly
145          150          155          160
Asp Gly Gln Glu Lys Asp Thr Gly Arg Asp Ile Glu Gly Glu Glu His
165          170          175
Thr Glu Ala Glu Ala Pro Thr Asn Ser Val Arg Glu His Ala Gly Thr
180          185          190
Ala Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Leu Arg Ala Ala Leu
195          200          205
Leu Gly Lys Phe Lys Glu Cys Phe Gly Leu Ser Phe Ile Asp Leu Ile
210          215          220

```

Arg	Pro	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Leu	Asp	Trp	Val	Val	Ala
225					230					235					240
Gly	Phe	Gly	Ile	His	His	Ser	Ile	Ser	Glu	Ala	Phe	Gln	Lys	Leu	Ile
				245					250					255	
Glu	Pro	Leu	Ser	Leu	Tyr	Ala	His	Ile	Gln	Trp	Leu	Thr	Asn	Ala	Trp
			260					265					270		
Gly	Met	Val	Leu	Leu	Val	Leu	Leu	Arg	Phe	Lys	Val	Asn	Lys	Ser	Arg
	275						280					285			
Ser	Thr	Val	Ala	Arg	Thr	Leu	Ala	Thr	Leu	Leu	Asn	Ile	Pro	Glu	Asn
	290					295					300				
Gln	Met	Leu	Ile	Glu	Pro	Pro	Lys	Ile	Gln	Ser	Gly	Val	Ala	Ala	Leu
305					310					315					320
Tyr	Trp	Phe	Arg	Thr	Gly	Ile	Ser	Asn	Ala	Ser	Thr	Val	Ile	Gly	Glu
				325					330					335	
Ala	Pro	Glu	Trp	Ile	Thr	Arg	Gln	Thr	Val	Ile	Glu	His	Gly	Leu	Ala
				340				345					350		
Asp	Ser	Gln	Phe	Lys	Leu	Thr	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp	Asn
		355					360				365				
Asp	Ile	Cys	Glu	Glu	Ser	Glu	Ile	Ala	Phe	Glu	Tyr	Ala	Gln	Arg	Gly
	370					375					380				
Asp	Phe	Asp	Ser	Asn	Ala	Arg	Ala	Phe	Leu	Asn	Ser	Asn	Met	Gln	Ala
385					390					395					400
Lys	Tyr	Val	Lys	Asp	Cys	Ala	Thr	Met	Cys	Arg	His	Tyr	Lys	His	Ala
				405					410					415	
Glu	Met	Arg	Lys	Met	Ser	Ile	Lys	Gln	Trp	Ile	Lys	His	Arg	Gly	Ser
			420					425					430		
Lys	Ile	Glu	Gly	Thr	Gly	Asn	Trp	Lys	Pro	Ile	Val	Gln	Phe	Leu	Arg
		435					440					445			
His	Gln	Asn	Ile	Glu	Phe	Ile	Pro	Phe	Leu	Thr	Lys	Phe	Lys	Leu	Trp
	450					455					460				
Leu	His	Gly	Thr	Pro	Lys	Lys	Asn	Cys	Ile	Ala	Ile	Val	Gly	Pro	Pro
465					470					475					480
Asp	Thr	Asp	Lys	Ser	Tyr	Phe	Cys	Met	Ser	Leu	Ile	Ser	Phe	Leu	Gly
				485					490					495	
Gly	Thr	Val	Ile	Ser	His	Val	Asn	Ser	Ser	Ser	His	Phe	Trp	Leu	Gln
			500					505					510		
Pro	Leu	Val	Asp	Ala	Lys	Val	Ala	Leu	Leu	Asp	Asp	Ala	Thr	Gln	Pro
		515					520					525			
Cys	Trp	Ile	Tyr	Met	Asp	Thr	Tyr	Met	Arg	Asn	Leu	Leu	Asp	Gly	Asn
	530					535					540				
Pro	Met	Ser	Ile	Asp	Arg	Lys	His	Lys	Ala	Leu	Thr	Leu	Ile	Lys	Cys
545					550					555					560
Pro	Pro	Leu	Leu	Val	Thr	Ser	Asn	Ile	Asp	Ile	Thr	Lys	Glu	Asp	Lys
				565					570					575	
Tyr	Lys	Tyr	Leu	His	Thr	Arg	Val	Thr	Thr	Phe	Thr	Phe	Pro	Asn	Pro
			580					585					590		
Phe	Pro	Phe	Asp	Arg	Asn	Gly	Asn	Ala	Val	Tyr	Glu	Leu	Ser	Asn	Thr
		595					600				605				
Asn	Trp	Lys	Cys	Phe	Phe	Glu	Arg	Leu	Ser	Ser	Ser	Leu	Asp	Ile	Gln
	610					615					620				
Asp	Ser	Glu	Asp	Glu	Glu	Asp	Gly	Ser	Asn	Ser	Gln	Ala	Phe	Arg	Cys
625					630					635					640
Val	Pro	Gly	Thr	Val	Val	Arg	Thr	Leu							
				645											

<210> 5  
 <211> 1104  
 <212> DNA

<213> hpv

<400> 5

```
atggaagcca tgcgaagag gctcgacgcc tgccaggacc agctgctcga gctgtacgag 60
gagaacagca ttgacatcca taagcacatc atgcaactgga agtgcattcg cctggagagc 120
gtgctgtttgc acaaggccaa gcagatgggc ctgtcccaca taggccttca ggtgggtccc 180
cctctgaccg tgtcagagac aaagggccat aacgcaatcg agatgcagat gcacctcgag 240
tcgctggcga aaacacagta cggcgtggag ccatggaccc tgcaggacac ctcgtacgaa 300
atgtggctga cccacaccta gcgatgcttc gccaaacagg gcaacacagt ggaggtgaag 360
ttcgacggct gtgaggataa cgttatggag tatgtcgtgt ggacgcacat ctatctgcag 420
gacaacgaca gttgggtgaa ggtgaccagc tccgtggacg cgaagggcat ctactatacc 480
tgtgggcagt ttaaaaccta ctatgtgaac ttcaacaaag agggccaaaa gtatggctcc 540
accaaccact gggaggtctg ctatgggagc acggtgattt gctctcccg cagcgtgtct 600
agcactgtgc gcgaggtgag cattgccgag ccgaccacgt acaccctgc ccagacgacc 660
gctccgaccg tgtctgcttg tactaccgag gacggcgtga gcgctccacc caggaagcgt 720
gcgagggggc caagcaccaa caacaccctc tgtgtggcga acattcgcag cgtcgacagt 780
accatcaata acatcgtgac ggataactat aacaagcacc agaggcgtaa caactgtcac 840
tctgccgcaa ccccatcgt gcagctccag ggagacagca attgccttaa gtgcttccgc 900
tatcgctca acgacaagta caagcacctc tttgagctcg cctcgtcgac gtggcactgg 960
gcctcaccg aggcacctca caagaacgcc atcgtcactc tcacttactc cagtgaggag 1020
cagagacagc agtttctgaa cagcgtgaag atcccaccga cgatccgtca taaggtcggc 1080
ttcatgtcac tgcattctct gtga 1104
```

<210> 6

<211> 367

<212> PRT

<213> HPV

<400> 6

```
Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Asp Gln Leu Leu
 1          5          10          15
Glu Leu Tyr Glu Glu Asn Ser Ile Asp Ile His Lys His Ile Met His
 20          25          30
Trp Lys Cys Ile Arg Leu Glu Ser Val Leu Leu His Lys Ala Lys Gln
 35          40          45
Met Gly Leu Ser His Ile Gly Leu Gln Val Val Pro Pro Leu Thr Val
 50          55          60
Ser Glu Thr Lys Gly His Asn Ala Ile Glu Met Met Gln Met His Leu Glu
 65          70          75          80
Ser Leu Ala Lys Thr Gln Tyr Gly Val Glu Pro Trp Thr Leu Gln Asp
 85          90          95
Thr Ser Tyr Glu Met Trp Leu Thr Pro Pro Lys Arg Cys Phe Ala Lys
100          105          110
Gln Gly Asn Thr Val Glu Val Lys Phe Asp Gly Cys Glu Asp Asn Val
115          120          125
Met Glu Tyr Val Val Trp Thr His Ile Tyr Leu Gln Asp Asn Asp Ser
130          135          140
Trp Val Lys Val Thr Ser Ser Val Asp Ala Lys Gly Ile Tyr Tyr Thr
145          150          155          160
Cys Gly Gln Phe Lys Thr Tyr Tyr Val Asn Phe Asn Lys Glu Ala Gln
165          170          175

Lys Tyr Gly Ser Thr Asn His Trp Glu Val Cys Tyr Gly Ser Thr Val
180          185          190
Ile Cys Ser Pro Ala Ser Val Ser Ser Thr Val Arg Glu Val Ser Ile
195          200          205
Ala Glu Pro Thr Thr Tyr Thr Pro Ala Gln Thr Thr Ala Pro Thr Val
210          215          220
Ser Ala Cys Thr Thr Glu Asp Gly Val Ser Ala Pro Pro Arg Lys Arg
```

225					230					235				240	
Ala	Arg	Gly	Pro	Ser	Thr	Asn	Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg
				245					250					255	
Ser	Val	Asp	Ser	Thr	Ile	Asn	Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys
			260					265					270		
His	Gln	Arg	Arg	Asn	Asn	Cys	His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln
		275					280				285				
Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn
	290					295					300				
Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp
305					310					315				320	
Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr
				325					330					335	
Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro
		340						345					350		
Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser	Leu	His	Leu	Leu	
		355					360					365			

<210> 7  
 <211> 1104  
 <212> DNA  
 <213> HPV

<400> 7

atggaagcca	tgcggaagag	gctcgacgcc	tgccaggacc	agctgctcga	gctgtacgag	60
gagaacagca	ttgacatcca	taagcacatc	atgcactgga	agtgcattcg	cctggagagc	120
gtgctgttgc	acaaggccaa	gcagatgggc	ctgtcccaca	taggccttca	ggtgggtccc	180
cctctgaccg	tgtcagagac	aaagggccat	aacgcaatcg	agatgcagat	gcacctcgag	240
tcgctggcga	aaacacagta	cggcgtggag	ccatggaccc	tgaggacac	ctcgtagcaa	300
atgtggctga	ccccacctaa	gcgatgcttc	gccaaacagg	gcaacacagt	ggagggtgaag	360
ttcgacggct	gtgaggataa	cgttatggag	tatgtcgtgt	ggacgcacat	ctatctgcag	420
gacaacgaca	gttggttgaa	ggtgaccagc	tccgtggacg	cgaagggcat	ctactatacc	480
tgtgggcagt	ttaaaacctt	ctatgtgaac	ttcaacaaag	aggcccaaaa	gtatgggtcc	540
accaaccact	gggaggtctg	ctatgggagc	acggtgattt	gctctcccgc	cagcgtgtct	600
agcactgtgc	gcgaggtgag	cattgccgag	ccgaccacgt	acacccctgc	ccagacgacc	660
gctccgaccg	tgtctgcttg	tactaccgag	gacggcgtga	gcgctccacc	caggaagcgt	720
gcgaggggcc	caagcaccaa	caacaccctc	tgtgtggcga	acattcgcag	cgtcgacagt	780
accatcaata	acatcgtgac	ggataactat	aacaagcacc	agaggcgtaa	caactgtcac	840
tctgccgcaa	cccccatcgt	gcagctccag	ggagacagca	attgccttaa	gtgcttccgc	900
tatcgcttca	acgacaagta	caagcacctc	tttgagctcg	cctcgtcgac	gtggcactgg	960
gcctcaccgc	aggcacctca	caagaacgcc	atcgtcactc	tcacttactc	cagtgaggag	1020
cagagacagc	agtttctgaa	cagcgtgaag	atcccaccga	cgatccgtca	taaggtcggc	1080
ttcatgtcac	tgcattctct	gtga				1104

<210> 8  
 <211> 367  
 <212> PRT  
 <213> HPV

<400> 8

Met	Glu	Ala	Ile	Ala	Lys	Arg	Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu
1				5					10					15	
Glu	Leu	Tyr	Glu	Glu	Asn	Ser	Ile	Asp	Ile	His	Lys	His	Ile	Met	His
			20					25					30		
Trp	Lys	Cys	Ile	Arg	Leu	Glu	Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln
		35					40				45				
Met	Gly	Leu	Ser	His	Ile	Gly	Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val
	50					55					60				

Ser	Glu	Thr	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	65	70	75	80
Ser	Leu	Ala	Lys	Thr	Gln	Tyr	Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp	85	90	95	
Thr	Ser	Tyr	Glu	Met	Trp	Leu	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	100	105	110	
Gln	Gly	Asn	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val	115	120	125	
Met	Glu	Tyr	Val	Val	Trp	Thr	His	Ile	Tyr	Leu	Gln	Asp	Asn	Asp	Ser	130	135	140	
Trp	Val	Lys	Val	Thr	Ser	Ser	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr	145	150	155	160
Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Asn	Lys	Glu	Ala	Gln	165	170	175	
Lys	Tyr	Gly	Ser	Thr	Asn	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val	180	185	190	
Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Val	Arg	Glu	Val	Ser	Ile	195	200	205	
Ala	Glu	Pro	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Thr	Ala	Pro	Thr	Val	210	215	220	
Ser	Ala	Cys	Thr	Thr	Glu	Asp	Gly	Val	Ser	Ala	Pro	Pro	Arg	Lys	Arg	225	230	235	240
Ala	Arg	Gly	Pro	Ser	Thr	Asn	Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg	245	250	255	
Ser	Val	Asp	Ser	Thr	Ile	Asn	Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys	260	265	270	
His	Gln	Arg	Arg	Asn	Asn	Cys	His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln	275	280	285	
Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn	290	295	300	
Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp	305	310	315	320
Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr	325	330	335	
Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro	340	345	350	
Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser	Leu	His	Leu	Leu		355	360	365	

<210> 9  
 <211> 2206  
 <212> DNA  
 <213> HPV

<400> 9  
 atggaagcta ttgccaagcg actggacgcc tgccaggagc agctgctgga gctgtacgag 60  
 gaaaacagca cagacctcca caagcacgtg ctgcaactgga agtgcattgcg ccacgagtca 120  
 gtgctcctgt acaaggccaa gcagatgggg ctgtcccaca tcgggatgca ggctcgtgcc 180  
 ccgctgaagg tgagcgaagc caagggccac aacgctatcg agatgcagat gcacctggag 240  
 agcctgctgc ggaccgaata cagcatggag ccctggactc tccaggagac gtcctacgaa 300  
 atgtggcaga ctccctccgaa gcgctgtttc gcaaagcgcg gcaagacagt tgaggtgaaa 360  
 ttgatgggt gcgcaaacaa cacgatggac tacgtggtgt ggaccgatgt ctacgtgcag 420  
 gacaatgaca cctgggtgaa ggtacatagt atggtggatg ccaagggcat ctattacacc 480  
 tgcgggcagt tcaagacgta ctacgtcaac ttctgcaagg aagccgaaaa gtatggttcc 540  
 accaagcact gggaggtgtg ttacgggagt actgtgatct gcagccccgc ctccgtgtcg 600  
 tccaccaccc aggaagtgag cattccggag agcaccacat acaccccgcc ccaaaccgagc 660  
 acgctcgtca gcagcagcac caaggaggac gccgtccaga cgcccccccg gaagagggcc 720  
 cgggggggtcc agcagttctc ctgcaatgcc ctgtgcgttg ctcacatcgg ccctgtcgat 780

```

tctgggaacc acaatctcat cacgaacaac caccgaccag accaaaggcg caacaactct 840
aacagctccg caactccaat agtgcagttc cagggggagt ccaactgcct caagtgtttc 900
cgctaccgcc tcaacgaccg ccaccgccac ctgttcgact tgatcagttc cactgtggcag 960
tgggccagca gcaaggcgcc ccacaaacac gctatcgtga cgggtgacct cgactccgag 1020
gagcagaggc agcagttcct ggacgtcgtg aagattcctc cgacaatcag ccacaagctt 1080
ggcttcatgt ccttgcacct gctgatggaa gccatcgaga agaggctcga cgcctgccag 1140
gaccagctgc tcgagctgta cgaggagaac agcattgaca tccataagca catcatgcac 1200
tggaagtgca ttcgcctgga gagcgtgctg ttgcacaagg ccaagcagat gggcctgtcc 1260
cacataggcc ttcagggtgt ccccccctctg accgtgtcag agacaaaggg ccataacgca 1320
atcgagatgc agatgcacct cgagtcgctg gcgaaaacac agtacggcgt ggagccatgg 1380
accctgcagg acacctcgta cgaaatgtgg ctgacccac ctaagcgatg cttcgccaaa 1440
cagggaaca cagtggaggt gaagtctgac ggctgtgagg ataacgttat ggagtatgtc 1500
gtgtggacgc acatctatct gcaggacaac gacagttggg tgaagggtgac cagctccgtg 1560
gacgcgaagg gcatctacta tacctgtggg cagtttaaaa cctactatgt gaacttcaac 1620
aaagaggccc aaaagtatgg ctccaccaac cactgggagg tctgctatgg gagcaggtg 1680
atttgctctc ccgccagcgt gtctagcact gtgcgcgagg tgagcattgc cgagccgacc 1740
acgtacaccc ctgccagac gaccgctccg accgtgtctg cttgtactac cgaggacggc 1800
gtgagcgctc caccagga gctgctgagg ggcccaagca ccaacaacac cctctgtgtg 1860
gcgaacattc gcagcgtcga cagtaccatc aataacatcg tgacggataa ctataacaag 1920
caccagaggc gtaacaactg tcaactctgc gcaaccccca tcgtgcagct ccaggagac 1980
agcaattgcc ttaagtgtt ccgctatcgc ctcaacgaca agtacaagca cctctttgag 2040
ctcgcctcgt cgacgtggca ctgggacctc cccgaggcac ctcacaagaa cgccatcgtc 2100
actctcactt actccagtga ggagcagaga cagcagtttc tgaacagcgt gaagatccca 2160
ccgacgatcc gtcataaggt cggcttcatg tcactgcac tctga 2206

```

<210> 10  
<211> 735  
<212> PRT  
<213> HPV

```

<400> 10
Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Glu Gln Leu Leu
 1          5          10          15
Glu Leu Tyr Glu Glu Asn Ser Thr Asp Leu His Lys His Val Leu His
 20          25          30
Trp Lys Cys Met Arg His Glu Ser Val Leu Leu Tyr Lys Ala Lys Gln
 35          40          45
Met Gly Leu Ser His Ile Gly Met Gln Val Val Pro Pro Leu Lys Val
 50          55          60
Ser Glu Ala Lys Gly His Asn Ala Ile Glu Met Gln Met His Leu Glu
 65          70          75          80
Ser Leu Leu Arg Thr Glu Tyr Ser Met Glu Pro Trp Thr Leu Gln Glu
 85          90          95
Thr Ser Tyr Glu Met Trp Gln Thr Pro Pro Lys Arg Cys Phe Ala Lys
100          105          110
Arg Gly Lys Thr Val Glu Val Lys Phe Asp Gly Cys Ala Asn Asn Thr
115          120          125
Met Asp Tyr Val Val Trp Thr Asp Val Tyr Val Gln Asp Asn Asp Thr
130          135          140
Trp Val Lys Val His Ser Met Val Asp Ala Lys Gly Ile Tyr Tyr Thr
145          150          155          160
Cys Gly Gln Phe Lys Thr Tyr Tyr Val Asn Phe Val Lys Glu Ala Glu
165          170          175
Lys Tyr Gly Ser Thr Lys His Trp Glu Val Cys Tyr Gly Ser Thr Val
180          185          190
Ile Cys Ser Pro Ala Ser Val Ser Ser Thr Thr Gln Glu Val Ser Ile
195          200          205
Pro Glu Ser Thr Thr Tyr Thr Pro Ala Gln Thr Ser Thr Leu Val Ser
210          215          220

```



Ser	Ser	Thr	Lys	Glu	Asp	Ala	Val	Gln	Thr	Pro	Pro	Arg	Lys	Arg	Ala
225					230					235					240
Arg	Gly	Val	Gln	Gln	Ser	Pro	Cys	Asn	Ala	Leu	Cys	Val	Ala	His	Ile
			245						250					255	
Gly	Pro	Val	Asp	Ser	Gly	Asn	His	Asn	Leu	Ile	Thr	Asn	Asn	His	Asp
			260					265					270		
Gln	His	Gln	Arg	Arg	Asn	Asn	Ser	Asn	Ser	Ser	Ala	Thr	Pro	Ile	Val
		275					280					285			
Gln	Phe	Gln	Gly	Glu	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu
	290					295				300					
Asn	Asp	Arg	His	Arg	His	Leu	Phe	Asp	Leu	Ile	Ser	Ser	Thr	Trp	His
305					310					315					320
Trp	Ala	Ser	Ser	Lys	Ala	Pro	His	Lys	His	Ala	Ile	Val	Thr	Val	Thr
				325					330					335	
Tyr	Asp	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile
			340					345					350		
Pro	Pro	Thr	Ile	Ser	His	Lys	Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu
		355					360					365			
Met	Glu	Ala	Ile	Ala	Lys	Arg	Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu
	370					375					380				
Glu	Leu	Tyr	Glu	Glu	Asn	Ser	Ile	Asp	Ile	His	Lys	His	Ile	Met	His
385					390					395					400
Trp	Lys	Cys	Ile	Arg	Leu	Glu	Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln
				405					410					415	
Met	Gly	Leu	Ser	His	Ile	Gly	Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val
			420					425					430		
Ser	Glu	Thr	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu
		435					440					445			
Ser	Leu	Ala	Lys	Thr	Gln	Tyr	Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp
	450					455					460				
Thr	Ser	Tyr	Glu	Met	Trp	Leu	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys
465					470					475					480
Gln	Gly	Asn	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val
			485						490					495	
Met	Glu	Tyr	Val	Val	Trp	Thr	His	Ile	Tyr	Leu	Gln	Asp	Asn	Asp	Ser
			500					505					510		
Trp	Val	Lys	Val	Thr	Ser	Ser	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr
		515					520					525			
Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Asn	Lys	Glu	Ala	Gln
	530					535					540				
Lys	Tyr	Gly	Ser	Thr	Asn	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val
545					550					555					560
Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Val	Arg	Glu	Val	Ser	Ile
				565					570					575	
Ala	Glu	Pro	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Thr	Ala	Pro	Thr	Val
			580					585					590		
Ser	Ala	Cys	Thr	Thr	Glu	Asp	Gly	Val	Ser	Ala	Pro	Pro	Arg	Lys	Arg
		595					600					605			
Ala	Arg	Gly	Pro	Ser	Thr	Asn	Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg
	610					615					620				
Ser	Val	Asp	Ser	Thr	Ile	Asn	Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys
625					630					635					640
His	Gln	Arg	Arg	Asn	Asn	Cys	His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln
				645					650					655	
Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn
		660					665					670			
Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp
		675					680					685			
Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr

690						695						700					
Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro		
705						710				715					720		
Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser	Leu	His	Leu	Leu			
				725					730					735			

<210> 11  
 <211> 2206  
 <212> DNA  
 <213> HPV

<400> 11

atggaagcca	tgcggaagag	gctcgacgcc	tgccaggacc	agctgctcga	gctgtacgag	60
gagaacagca	ttgacatcca	taagcacatc	atgcactgga	agtgcattcg	cctggagagc	120
gtgctgttgc	acaaggccaa	gcagatgggc	ctgtcccaca	taggccttca	ggtgggtcccc	180
cctctgaccg	tgtcagagac	aaagggccat	aacgcaatcg	agatgcagat	gcacctcgag	240
tcgctggcga	aaacacagta	cggcgtggag	ccatggaccc	tgcaggacac	ctcgtacgaa	300
atgtggctga	ccccaccta	gcgatgcttc	gccaaacagg	gcaacacagt	ggaggtgaag	360
ttcgacggct	gtgaggataa	cgttatggag	tatgtcgtgt	ggacgcacat	ctatctgcag	420
gacaacgaca	gttgggtgaa	ggtgaccagc	tccgtggacg	cgaagggcat	ctactatacc	480
tgtgggcagt	ttaaaacct	ctatgtgaac	ttcaacaaag	aggcccaaaa	gtatggctcc	540
accaaccact	gggaggtctg	ctatgggagc	acggtgattt	gctctcccg	cagcgtgtct	600
agcactgtgc	gcgaggtgag	cattgccgag	ccgaccacgt	acacccctgc	ccagacgacc	660
gctccgaccg	tgtctgcttg	tactaccgag	gacggcgtga	gcgctccacc	caggaagcgt	720
gcgaggggccc	caagcaccaa	caacaccctc	tgtgtggcga	acattcgag	cgctgcacgt	780
accatcaata	acatcgtgac	ggataactat	aacaagcacc	agaggcgtaa	caactgtcac	840
tctgccgcaa	cccccatcgt	gcagctccag	ggagacagca	attgccttaa	gtgcttccgc	900
tatcgctcca	acgacaagta	caagcacctc	tttagctcgc	cctcgctcgac	gtggcactgg	960
gcctcaccgc	aggcacctca	caagaacgcc	atcgctactc	tcacttactc	cagtgaggag	1020
cagagacagc	agttttctgaa	cagcgtgaag	atcccaccga	cgatccgtca	taaggtcggc	1080
ttcatgtcac	tgcattctct	gatggaagct	attgccaagc	gactggacgc	ctgccaggag	1140
cagctgctgg	agctgtacga	ggaaaacagc	acagacctcc	acaagcacgt	gctgcactgg	1200
aagtgcattg	gccacgagtc	agtgtctcct	tacaaggcca	agcagatggg	gctgtcccac	1260
atcgggatgc	aggctcgtgc	cccgtctgaag	gtgagcgaag	ccaagggcca	caacgctatc	1320
gagatgcaga	tgcacctgga	gagcctgctg	cggaccgaat	acagcatgga	gccctggact	1380
ctccaggaga	cgctctacga	aatgtggcag	actcctccga	agcgtgtgtt	cgcaaagcgc	1440
ggcaagagag	ttgaggtgaa	attcgatggg	tgcgcaaaca	acacgatgga	ctacgtgggtg	1500
tggaccgatg	tctacgtgca	ggacaatgac	acctgggtga	aggtacatag	tatggtggat	1560
gccaaaggca	tctattacac	ctgcggggcag	ttcaagacgt	actacgtcaa	cttcgtcaag	1620
gaagccgaaa	agtatggttc	caccaagcac	tgggaggtgt	gttacgggag	tactgtgatc	1680
tgcagccccg	cctccgtgtc	gtccaccacc	caggaagtga	gcattccgga	gagcaccaca	1740
tacaccccg	cccaaacgag	cacgctcgtc	agcagcagca	ccaaggagga	cgccgtccag	1800
acgccccccc	ggaagagggc	ccgggggggtc	cagcagtctc	cctgcaatgc	cctgtgcgtt	1860
gtcacatcgc	gccctgtcga	ttctgggaac	cacaatctca	tcacgaacaa	ccacgaccag	1920
caccaaaggc	gcaacaactc	taacagctcc	gcaactccaa	tagtgcagtt	ccagggggag	1980
tccaactgcc	tcaagtgttt	ccgctaccgc	ctcaacgacc	gccaccgcca	cctgttcgac	2040
ttgatcagtt	ccacgtggca	ctggggccagc	agcaaggcgc	cccacaaaca	cgctatcgtg	2100
acggtgacct	acgactccga	ggagcagagg	cagcagttcc	tggacgtcgt	gaagattcct	2160
ccgacaatca	gccacaagct	tggcttcatg	tcctgcacc	tgctga		2206

<210> 12  
 <211> 735  
 <212> PRT  
 <213> HPV

<400> 12

Met	Glu	Ala	Ile	Ala	Lys	Arg	Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu
1				5					10					15	

Glu	Leu	Tyr	Glu	Glu	Asn	Ser	Ile	Asp	Ile	His	Lys	His	Ile	Met	His
			20					25					30		
Trp	Lys	Cys	Ile	Arg	Leu	Glu	Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln
		35					40					45			
Met	Gly	Leu	Ser	His	Ile	Gly	Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val
	50					55					60				
Ser	Glu	Thr	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu
65					70					75					80
Ser	Leu	Ala	Lys	Thr	Gln	Tyr	Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp
			85						90					95	
Thr	Ser	Tyr	Glu	Met	Trp	Leu	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys
			100					105					110		
Gln	Gly	Asn	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val
		115					120					125			
Met	Glu	Tyr	Val	Val	Trp	Thr	His	Ile	Tyr	Leu	Gln	Asp	Asn	Asp	Ser
	130					135					140				
Trp	Val	Lys	Val	Thr	Ser	Ser	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr
145					150					155					160
Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Asn	Lys	Glu	Ala	Gln
			165						170					175	
Lys	Tyr	Gly	Ser	Thr	Asn	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val
			180					185					190		
Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Val	Arg	Glu	Val	Ser	Ile
		195					200					205			
Ala	Glu	Pro	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Thr	Ala	Pro	Thr	Val
	210					215					220				
Ser	Ala	Cys	Thr	Thr	Glu	Asp	Gly	Val	Ser	Ala	Pro	Pro	Arg	Lys	Arg
225					230					235					240
Ala	Arg	Gly	Pro	Ser	Thr	Asn	Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg
			245						250					255	
Ser	Val	Asp	Ser	Thr	Ile	Asn	Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys
			260					265					270		
His	Gln	Arg	Arg	Asn	Asn	Cys	His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln
		275					280					285			
Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn
	290					295					300				
Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp
305					310					315					320
Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr
			325						330					335	
Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro
		340						345					350		
Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser	Leu	His	Leu	Leu	Met
		355					360					365			
Glu	Ala	Ile	Ala	Lys	Arg	Leu	Asp	Ala	Cys	Gln	Glu	Gln	Leu	Leu	Glu
	370					375					380				
Leu	Tyr	Glu	Glu	Asn	Ser	Thr	Asp	Leu	His	Lys	His	Val	Leu	His	Trp
385					390					395					400
Lys	Cys	Met	Arg	His	Glu	Ser	Val	Leu	Leu	Tyr	Lys	Ala	Lys	Gln	Met
			405						410					415	
Gly	Leu	Ser	His	Ile	Gly	Met	Gln	Val	Val	Pro	Pro	Leu	Lys	Val	Ser
			420					425					430		
Glu	Ala	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	Ser
	435					440					445				
Leu	Leu	Arg	Thr	Glu	Tyr	Ser	Met	Glu	Pro	Trp	Thr	Leu	Gln	Glu	Thr
	450					455					460				
Ser	Tyr	Glu	Met	Trp	Gln	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	Arg
465					470					475					480
Gly	Lys	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Ala	Asn	Asn	Thr	Met



```

aaatacgttaa aagactgctg taccatgtgc cgtcactaca aacacgcgga aatgcgtaaa 1260
atgtctatca aacagtggat caagcaccgc gggtctaaaa tcgaaggtag cggtaactgg 1320
aaaccgatcg ttcagttcct gcgccatcag aacatcgaat tcatcccggt cctgaccaa 1380
ttcaagctgt ggctgcacgg taccgccaaa aaaaactgca tcgtatcgt aggtccaccg 1440
gacactgaca agtcttactt ctgtatgtcc ctgatctctt tcctgggcgg cactgtaatc 1500
tctcacgtta actcttcctc ccatttctgg ctgcagccac tggtagacgc gaaagtagct 1560
ctgctggacg acgcgaccca gccgtgctgg atctacatgg atacttacat gcgcaacctg 1620
ctggacggta acccgatgtc tatcgaccgt aaacacaaaag cgctgactct gatcaagtgc 1680
ccgccgctgc tggtaacttc taacatcgac atcaccaagg aagataaata caagtacctg 1740
cataccgctg ttactacctt tactttcccg aaccggttcc cgtttgatcg taacggtaac 1800
gctgtttacg aactgtccaa cactaactgg aaatgcttct tcgagcgtct gtcttccctc 1860
ctggacatcc aggactctga agatgaagaa gatggttcta actctcaggc tttccgttgt 1920
gttccgggta ctgttggtcg tactctgtga 1950

```

<210> 14  
 <211> 649  
 <212> PRP  
 <213> HPV

<400> 14

Met	Ala	Asp	Asp	Ser	Gly	Thr	Glu	Asn	Glu	Gly	Ser	Gly	Cys	Thr	Gly
1				5					10					15	
Trp	Phe	Met	Val	Glu	Ala	Ile	Val	Gln	His	Pro	Thr	Gly	Thr	Gln	Ile
			20					25					30		
Ser	Asp	Asp	Glu	Asp	Glu	Glu	Val	Glu	Asp	Ser	Gly	Tyr	Asp	Met	Val
		35				40						45			
Asp	Phe	Ile	Asp	Asp	Ser	Asn	Ile	Thr	His	Asn	Ser	Leu	Glu	Ala	Gln
	50				55					60					
Ala	Leu	Phe	Asn	Arg	Gln	Glu	Ala	Asp	Thr	His	Tyr	Ala	Thr	Val	Gln
65					70					75					80
Asp	Leu	Gly	Gly	Lys	Tyr	Leu	Gly	Ser	Pro	Tyr	Val	Ser	Pro	Ile	Asn
				85				90						95	
Thr	Ile	Ala	Glu	Ala	Val	Glu	Ser	Glu	Ile	Ser	Pro	Arg	Leu	Asp	Ala
			100					105					110		
Ile	Lys	Leu	Thr	Arg	Gln	Pro	Lys	Lys	Val	Lys	Arg	Arg	Leu	Phe	Gln
	115					120					125				
Thr	Arg	Glu	Leu	Thr	Asp	Ser	Gly	Tyr	Gly	Tyr	Ser	Glu	Val	Glu	Ala
	130					135					140				
Gly	Thr	Gly	Thr	Gln	Val	Glu	Lys	His	Gly	Val	Pro	Glu	Asn	Gly	Gly
145					150					155					160
Asp	Gly	Gln	Glu	Lys	Asp	Thr	Gly	Arg	Asp	Ile	Glu	Gly	Glu	Glu	His
				165				170						175	
Thr	Glu	Ala	Glu	Ala	Pro	Thr	Asn	Ser	Val	Arg	Glu	His	Ala	Gly	Thr
			180					185					190		
Ala	Gly	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Lys	Asp	Leu	Arg	Ala	Ala	Leu
	195						200				205				
Leu	Gly	Lys	Phe	Lys	Glu	Cys	Phe	Gly	Leu	Ser	Phe	Ile	Asp	Leu	Ile
	210					215					220				
Arg	Pro	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Leu	Asp	Trp	Val	Val	Ala
225					230					235					240
Gly	Phe	Gly	Ile	His	His	Ser	Ile	Ser	Glu	Ala	Phe	Gln	Lys	Leu	Ile
				245					250						255
Glu	Pro	Leu	Ser	Leu	Tyr	Ala	His	Ile	Gln	Trp	Leu	Thr	Asn	Ala	Trp
			260					265					270		
Gly	Met	Val	Leu	Leu	Val	Leu	Leu	Arg	Phe	Lys	Val	Asn	Lys	Ser	Arg
		275					280					285			
Ser	Thr	Val	Ala	Arg	Thr	Leu	Ala	Thr	Leu	Leu	Asn	Ile	Pro	Glu	Asn
	290					295					300				
Gln	Met	Leu	Ile	Glu	Pro	Pro	Lys	Ile	Gln	Ser	Gly	Val	Ala	Ala	Leu

305					310					315				320
Tyr	Trp	Phe	Arg	Thr	Gly	Ile	Ser	Asn	Ala	Ser	Thr	Val	Ile	Gly
				325					330					335
Ala	Pro	Glu	Trp	Ile	Thr	Arg	Gln	Thr	Val	Ile	Glu	His	Gly	Leu
			340					345					350	
Asp	Ser	Gln	Phe	Lys	Leu	Thr	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp
	355						360				365			Asn
Asp	Ile	Cys	Glu	Glu	Ser	Glu	Ile	Ala	Phe	Glu	Tyr	Ala	Gln	Arg
	370					375					380			Gly
Asp	Phe	Asp	Ser	Asn	Ala	Arg	Ala	Phe	Leu	Asn	Ser	Asn	Met	Gln
385					390					395				400
Lys	Tyr	Val	Lys	Asp	Cys	Ala	Thr	Met	Cys	Arg	His	Tyr	Lys	His
			405					410						415
Glu	Met	Arg	Lys	Met	Ser	Ile	Lys	Gln	Trp	Ile	Lys	His	Arg	Gly
	420							425					430	Ser
Lys	Ile	Glu	Gly	Thr	Gly	Asn	Trp	Lys	Pro	Ile	Val	Gln	Phe	Leu
	435					440						445		Arg
His	Gln	Asn	Ile	Glu	Phe	Ile	Pro	Phe	Leu	Thr	Lys	Phe	Lys	Leu
	450					455				460				Trp
Leu	His	Gly	Thr	Pro	Lys	Lys	Asn	Cys	Ile	Ala	Ile	Val	Gly	Pro
465					470				475					480
Asp	Thr	Asp	Lys	Ser	Tyr	Phe	Cys	Met	Ser	Leu	Ile	Ser	Phe	Leu
			485					490						495
Gly	Thr	Val	Ile	Ser	His	Val	Asn	Ser	Ser	Ser	His	Phe	Trp	Leu
			500				505						510	Gln
Pro	Leu	Val	Asp	Ala	Lys	Val	Ala	Leu	Leu	Asp	Asp	Ala	Thr	Gln
	515					520						525		Pro
Cys	Trp	Ile	Tyr	Met	Asp	Thr	Tyr	Met	Arg	Asn	Leu	Leu	Asp	Gly
	530					535				540				Asn
Pro	Met	Ser	Ile	Asp	Arg	Lys	His	Lys	Ala	Leu	Thr	Leu	Ile	Lys
545				550					555					560
Pro	Pro	Leu	Leu	Val	Thr	Ser	Asn	Ile	Asp	Ile	Thr	Lys	Glu	Asp
			565					570						575
Tyr	Lys	Tyr	Leu	His	Thr	Arg	Val	Thr	Thr	Phe	Thr	Phe	Pro	Asn
			580					585					590	Pro
Phe	Pro	Phe	Asp	Arg	Asn	Gly	Asn	Ala	Val	Tyr	Glu	Leu	Ser	Asn
	595					600					605			Thr
Asn	Trp	Lys	Cys	Phe	Phe	Glu	Arg	Leu	Ser	Ser	Ser	Leu	Asp	Ile
	610					615					620			Gln
Asp	Ser	Glu	Asp	Glu	Glu	Asp	Gly	Ser	Asn	Ser	Gln	Ala	Phe	Arg
625				630					635					640
Val	Pro	Gly	Thr	Val	Val	Arg	Thr	Leu						
				645										

<210> 15  
 <211> 1107  
 <212> DNA  
 <213> HPV

<400> 15  
 atggaagcta ttgccaagcg actggacgcc tgccaggagc agctgctgga gctgtacgag 60  
 gaaaacagca cagacctcca caagcacgtg ctgcactgga agtgcattgcg ccacgagtca 120  
 gtgctcctgt acaaggccaa gcagatgggg ctgtcccaca tcgggatgca ggctcgtgcc 180  
 ccgctgaagg tgagcgaagc caagggccac aacgctatcg agatgcagat gcacctggag 240  
 agcctgctgc ggaccgaata cagcatggag ccttgactc tccaggagac gtcctacgaa 300  
 atgtggcaga ctctccgaa gcgctgtttc gcaaagcgcg gcaagacagt tgaggtgaaa 360  
 ttcgatgggt gcgcaaaca cagcatggac tacgtggtgt ggaccgatgt ctacgtgcag 420  
 gacaatgaca cctgggtgaa ggtacatagt atggtggatg ccaagggcat ctattacacc 480

```

tgcgggcagt tcaagacgta ctacgtcaac ttcgtcaagg aagccgaaaa gtatgggttcc 540
accaagcact gggagggtgtg ttacgggagt actgtgatct gcagccccgc ctccgtgtcg 600
tccaccaccc aggaagtgtg cattccggag agcaccacat acacccccgc ccaaacgagc 660
acgctcgtca gcagcagcac caaggaggac gccgtccaga cgcacccccg gaagagggcc 720
cgggggggtcc agcagtctcc ctgcaatgcc ctgtgcgttg ctcacatcgg ccctgtcgat 780
tctgggaacc acaatctcat cacgaacaac cagcaccagc accaaaggcg caacaactct 840
aacagctccg caactccaat agtgcagttc cagggggagt ccaactgcct caagtgtttc 900
cgctaccgcc tcaacgaccg ccaccgccac ctgttcgact tgatcagttc cacgtggcac 960
tgggccagca gcaaggcgcc ccacaaacac gctatcgtga cggtgacctc cgactccgag 1020
gagcagaggc agcagttcct ggacgtcgtg aagattcctc cgacaatcag ccacaagctt 1080
ggcttcatgt cctgcacct gctgtga 1107

```

<210> 16  
 <211> 368  
 <212> PRT  
 <213> HPV

```

<400> 16
Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Glu Gln Leu Leu
 1          5          10          15
Glu Leu Tyr Glu Glu Asn Ser Thr Asp Leu His Lys His Val Leu His
 20          25          30
Trp Lys Cys Met Arg His Glu Ser Val Leu Leu Tyr Lys Ala Lys Gln
 35          40          45
Met Gly Leu Ser His Ile Gly Met Gln Val Val Pro Pro Leu Lys Val
 50          55          60
Ser Glu Ala Lys Gly His Asn Ala Ile Glu Met Gln Met His Leu Glu
 65          70          75          80
Ser Leu Leu Arg Thr Glu Tyr Ser Met Glu Pro Trp Thr Leu Gln Glu
 85          90          95
Thr Ser Tyr Glu Met Trp Gln Thr Pro Pro Lys Arg Cys Phe Ala Lys
100          105          110
Arg Gly Lys Thr Val Glu Val Lys Phe Asp Gly Cys Ala Asn Asn Thr
115          120          125
Met Asp Tyr Val Val Trp Thr Asp Val Tyr Val Gln Asp Asn Asp Thr
130          135          140
Trp Val Lys Val His Ser Met Val Asp Ala Lys Gly Ile Tyr Tyr Thr
145          150          155          160
Cys Gly Gln Phe Lys Thr Tyr Tyr Val Asn Phe Val Lys Glu Ala Glu
165          170          175
Lys Tyr Gly Ser Thr Lys His Trp Glu Val Cys Tyr Gly Ser Thr Val
180          185          190
Ile Cys Ser Pro Ala Ser Val Ser Ser Thr Thr Gln Glu Val Ser Ile
195          200          205
Pro Glu Ser Thr Thr Tyr Thr Pro Ala Gln Thr Ser Thr Leu Val Ser
210          215          220
Ser Ser Thr Lys Glu Asp Ala Val Gln Thr Pro Pro Arg Lys Arg Ala
225          230          235          240
Arg Gly Val Gln Gln Ser Pro Cys Asn Ala Leu Cys Val Ala His Ile
245          250          255
Gly Pro Val Asp Ser Gly Asn His Asn Leu Ile Thr Asn Asn His Asp
260          265          270
Gln His Gln Arg Arg Asn Asn Ser Asn Ser Ser Ala Thr Pro Ile Val
275          280          285
Gln Phe Gln Gly Glu Ser Asn Cys Leu Lys Cys Phe Arg Tyr Arg Leu
290          295          300
Asn Asp Arg His Arg His Leu Phe Asp Leu Ile Ser Ser Thr Trp His
305          310          315          320
Trp Ala Ser Ser Lys Ala Pro His Lys His Ala Ile Val Thr Val Thr

```

			325							330					335
Tyr	Asp	Ser	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile	
			340					345				350			
Pro	Pro	Thr	Ile	Ser	His	Lys	Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu
		355					360					365			

<210> 17  
 <211> 4154  
 <212> DNA  
 <213> HPV

<400> 17

atggcagacg	attccgggtac	tgagaacgaa	ggttctgggtt	gtaccgggttg	gttcatgggtt	60
gaagcaatcg	ttcagcatcc	gactgggtacc	cagatctccg	atgacgaaga	cgaagaagtt	120
gaagattctg	gttacgacat	ggttgacttc	atcgatgact	ccaacatcac	tcataactct	180
ctggaagcac	aggctctgtt	taaccgccag	gaagctgata	cccattacgc	tactgttcag	240
gacctgggag	gcaaatatct	gggctctccg	tacgtttccc	cgatcaacac	tatcgcagaa	300
gcagttgagt	ctgaaatctc	cccgcgcctg	gacgctatca	aactgactcg	tcagccgaag	360
aaggttaaac	gtcgtctgtt	ccagactcgt	gaactgaccg	actccgggta	cggttatagc	420
gaagttgagg	ctggcaccgg	cacccaggtt	gaaaaacacg	gtgtaccgga	aaacggcggc	480
gacggtcagg	aaaaggacac	cggccgcgac	atcgagggtg	aggaacacac	cgaagctgaa	540
gctccgacta	actctgttcg	tgaacacgca	ggtactgcgg	gtatcctgga	actgctgaaa	600
tgcaaagacc	tgcgcgcggc	tctgctgggc	aaattcaaag	aatgcttcgg	cctgtctttc	660
attgacctga	tccgtccggt	taagtctgac	aaaactacct	gtctgggactg	ggttgtagca	720
ggcttcggca	tcaccactc	tatctctgaa	gcattccaga	aactgatcga	gccgctgtct	780
ctgtacgcgc	acatccagtg	gctgactaac	gcttggggta	tggttctgct	ggtagctgtc	840
cgctttaaag	taaacaaatc	tcgttccact	gttgctcgta	ctctgggtac	cctgtgaac	900
atcccgagga	accagatgct	gatcgaaccg	ccgaaaatcc	agtctggtgt	agctgcactg	960
tactggtttc	gtactggcat	ctctaaccgt	agcactgtta	tcgggtgaagc	accggaatgg	1020
atcactcgtc	agaccgttat	cgaacacggg	ctggcagatt	ctcagttcaa	actgactgaa	1080
atggttcagt	gggcatacga	caacgacatc	tgcgaggaat	ctgaaattgc	gttcgaatac	1140
gctcagcgctg	gcgacttcga	ctccaacgct	cgtgctttcc	tgaacagcaa	catgcaggct	1200
aaatacgtaa	aagactgcgc	taccatgtgc	cgctactaca	aacacgcgga	aatgcgtaaa	1260
atgtctatca	aacagtggat	caagcaccgc	ggttctaaaa	tcgaaggtag	cggtaactgg	1320
aaaccgatcg	ttcagttcct	gcgccatcag	aacatcgaat	tcatcccgtt	cctgaccaa	1380
ttcaagctgt	ggctgcacgg	taccccga	aaaaactgca	tcgctatcgt	aggtccaccg	1440
gacactgaca	agtcttactt	ctgtatgtcc	ctgatctctt	tcctggggcg	cactgtaatc	1500
tctcacgtta	actcttcttc	ccatttctgg	ctgcagccac	tggtagacgc	gaaagtagct	1560
ctgctggacg	acgcgaccca	gccgtgctgg	atctacatgg	atacttacat	gcgcaacctg	1620
ctggacggta	acccgatgtc	tatcgaccgt	aaacacaaag	cgctgactct	gatcaagtgc	1680
ccgccgctgc	tggttaactt	taacatcgac	atcaccaagg	aagataaata	caagtacctg	1740
catacccgctg	ttactacctt	tactttcccc	aaccggttcc	cgtttgatcg	taacggtaac	1800
gctgtttacg	aactgtccaa	cactaactgg	aaatgcttct	tcgagcgtct	gtcttctctc	1860
ctggacatcc	aggactctga	agatgaagaa	gatggttcta	actctcaggc	tttccggttg	1920
gttccgggta	ctgttggtcg	tactctgatg	gaagctattg	ccaagcgact	ggacgcctgc	1980
caggagcagc	tgctggagct	gtacgaggaa	aacagcacag	acctccacaa	gcacgtgctg	2040
cactggaagt	gcatgcgcca	cgagtcagtg	ctcctgtaca	aggccaagca	gatggggctg	2100
tcccacatcg	ggatgcagggt	cgtgcccccg	ctgaagggtga	gcgaagccaa	gggccacaac	2160
gctatcgaga	tgcagatgca	cctggagagc	ctgctgcgga	ccgaatacag	catggagccc	2220
tggactctcc	aggagacgtc	ctacgaaatg	tggcagactc	ctccgaagcg	ctgtttcgca	2280
aagcgcggca	agacagttga	ggtgaaattc	gatgggtgcg	caaacaacac	gatggactac	2340
gtggtgtgga	ccgatgtcta	cgtgcaggac	aatgacacct	gggtgaagggt	acatagtatg	2400
gtggatgcca	agggcatcta	ttacacctgc	gggcagttca	agacgtacta	cgtcaacttc	2460
gtcaagggaag	cgtaaaagta	tggttccacc	aagcactggg	aggtgtgtta	cgggagtaac	2520
gtgatctgca	gccccgcctc	cgtgtcgtcc	accacccagg	aagttagcat	tcgggagaga	2580
ccacatacac	cccgccccaa	acgagcacgc	tcgtcagcag	cagcaccaag	gaggacgccc	2640
tccagacgcc	cccccggaag	agggccccgg	gggtccagca	gtctccctgc	aatgccctgt	2700



```

gcgttgctca catcggccct gtcgattctg ggaaccacaa tctcatcacg aacaaccacg 2760
accagcacca aaggcgcaac aactctaaca gctccgcaac tccaatagtg cagttccagg 2820
gggagtccaa ctgcctcaag tgtttccgct accgcctcaa cgaccgccac cgccacctgt 2880
tcgacttgat cagttccacg tggcactggg ccagcagcaa ggcgccccac aaacacgcta 2940
tcgtgacggt gacctacgac tccgaggagc agaggcagca gttcctggac gtcgtgaaga 3000
ttcctccgac aatcagccac aagcttggct tcatgtccct gcacctgctg atggaagcca 3060
tcgcgaagag gctcgacgcc tgccaggacc agctgctcga gctgtacgag gagaacagca 3120
ttgacatcca taagcacatc atgcactgga agtgcattcg cctggagagc gtgctgttgc 3180
acaaggccaa gcagatgggc ctgtcccaca taggccttca ggtgggtcccc cctctgaccg 3240
tgtcagagac aaagggccat aacgcaatcg agatgcagat gcacctcgag tcgctggcga 3300
aaacacagta cggcgtggag ccatggaccc tgcaggacac ctcgtacgaa atgtggctga 3360
ccccacctaa gcgatgcttc gccaaacagg gcaacacagt ggaggtgaag ttcgacggct 3420
gtgaggataa cgttatggag tatgtcgtgt ggacgcacat ctatctgcag gacaacgaca 3480
gttgggtgaa ggtgaccagc tccgtggacg cgaagggcat ctactatacc tgtgggcagt 3540
ttaaaaccta ctatgtgaac ttcaacaaag aggcccaaaa gtatggctcc accaaccact 3600
gggaggtctg ctatgggagc acggtgattt gctctcccg cagcgtgtct agcactgtgc 3660
gcgaggtgag cattgccgag ccgaccacgt acaccctgc ccagacgacc gctccgaccg 3720
tgtctgcttg tactaccgag gacggcgtga gcgctccacc caggaagcgt gcgaggggcc 3780
caagcaccaa caacaccctc tgtgtggcga acattcgag cgctcgacagt accatcaata 3840
acatcgtgac ggataactat aacaagcacc agaggcgtaa caactgtcac tctgccgcaa 3900
ccccatcgt gcagctccag ggagacagca attgccttaa gtgcttccgc tatcgcttca 3960
acgacaagta caagcacctc tttgagctcg cctcgtcgac gtggcactgg gcctcaccgc 4020
aggcacctca caagaacgcc atcgtcactc tcacttactc cagtgaggag cagagacagc 4080
agtttctgaa cagcgtgaag atcccaccga cgatccgtca taaggtcggc ttcatgtcac 4140
tgcattcct gtga 4154

```

<210> 18  
 <211> 1384  
 <212> PRT  
 <213> HPV

```

<400> 18
Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
 1          5          10          15
Trp Phe Met Val Glu Ala Ile Val Gln His Pro Thr Gly Thr Gln Ile
 20          25          30
Ser Asp Asp Glu Asp Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
 35          40          45
Asp Phe Ile Asp Asp Ser Asn Ile Thr His Asn Ser Leu Glu Ala Gln
 50          55          60
Ala Leu Phe Asn Arg Gln Glu Ala Asp Thr His Tyr Ala Thr Val Gln
 65          70          75          80
Asp Leu Gly Gly Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Asn

          85          90          95
Thr Ile Ala Glu Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
 100          105          110
Ile Lys Leu Thr Arg Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Gln
 115          120          125
Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
 130          135          140
Gly Thr Gly Thr Gln Val Glu Lys His Gly Val Pro Glu Asn Gly Gly
 145          150          155          160
Asp Gly Gln Glu Lys Asp Thr Gly Arg Asp Ile Glu Gly Glu Glu His
          165          170          175
Thr Glu Ala Glu Ala Pro Thr Asn Ser Val Arg Glu His Ala Gly Thr
 180          185          190
Ala Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Leu Arg Ala Ala Leu
 195          200          205

```

Leu 210	Gly	Lys	Phe	Lys	Glu	Cys	Phe	Gly	Leu	Ser	Phe	Ile	Asp	Leu	Ile
Arg 225	Pro	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Leu	Asp	Trp	Val	Val	Ala
Gly	Phe	Gly	Ile	His 245	His	Ser	Ile	Ser	Glu 250	Ala	Phe	Gln	Lys	Leu 255	Ile
Glu	Pro	Leu	Ser	Leu 260	Tyr	Ala	His	Ile	Gln 265	Trp	Leu	Thr	Asn	Ala	Trp
Gly	Met	Val	Leu	Leu	Val	Leu	Leu	Arg	Phe	Lys	Val	Asn	Lys	Ser	Arg
Ser	Thr	Val	Ala	Arg	Thr	Leu	Ala	Thr	Leu	Leu	Asn	Ile	Pro	Glu	Asn
Gln 305	Met	Leu	Ile	Glu	Pro	Pro	Lys	Ile	Gln	Ser	Gly	Val	Ala	Ala	Leu
Tyr	Trp	Phe	Arg	Thr 325	Gly	Ile	Ser	Asn	Ala	Ser	Thr	Val	Ile	Gly	Glu
Ala	Pro	Glu	Trp	Ile 340	Thr	Arg	Gln	Thr	Val	Ile	Glu	His	Gly	Leu	Ala
Asp	Ser	Gln	Phe	Lys	Leu	Thr	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp	Asn
Asp	Ile	Cys	Glu	Glu	Ser	Glu	Ile	Ala	Phe	Glu	Tyr	Ala	Gln	Arg	Gly
Asp	Phe	Asp	Ser	Asn	Ala	Arg	Ala	Phe	Leu	Asn	Ser	Asn	Met	Gln	Ala
385					390					395					400
Lys	Tyr	Val	Lys	Asp 405	Cys	Ala	Thr	Met	Cys 410	Arg	His	Tyr	Lys	His	Ala
Glu	Met	Arg	Lys	Met 420	Ser	Ile	Lys	Gln	Trp 425	Ile	Lys	His	Arg	Gly	Ser
Lys	Ile	Glu	Gly	Thr 435	Gly	Asn	Trp	Lys	Pro	Ile	Val	Gln	Phe	Leu	Arg
His	Gln	Asn	Ile	Glu	Phe	Ile	Pro	Phe	Leu	Thr	Lys	Phe	Lys	Leu	Trp
Leu 465	His	Gly	Thr	Pro	Lys 470	Lys	Asn	Cys	Ile	Ala	Ile	Val	Gly	Pro	Pro
Asp	Thr	Asp	Lys	Ser	Tyr	Phe	Cys	Met	Ser 490	Leu	Ile	Ser	Phe	Leu	Gly
Gly	Thr	Val	Ile	Ser	His	Val	Asn	Ser	Ser 505	Ser	His	Phe	Trp	Leu	Gln
Pro	Leu	Val	Asp	Ala	Lys	Val	Ala	Leu	Leu	Asp	Asp	Ala	Thr	Gln	Pro
Cys	Trp	Ile	Tyr	Met	Asp	Thr	Tyr	Met	Arg	Asn	Leu	Asp	Gly	Asn	
Pro 545	Met	Ser	Ile	Asp	Arg	Lys	His	Lys	Ala	Leu	Thr	Leu	Ile	Lys	Cys
Pro	Pro	Leu	Leu	Val	Thr	Ser	Asn	Ile	Asp	Ile	Thr	Lys	Glu	Asp	Lys
Tyr	Lys	Tyr	Leu	His	Thr	Arg	Val	Thr	Thr	Phe	Thr	Phe	Pro	Asn	Pro
Phe	Pro	Phe	Asp	Arg	Asn	Gly	Asn	Ala	Val	Tyr	Glu	Leu	Ser	Asn	Thr
Asn	Trp	Lys	Cys	Phe	Phe	Glu	Arg	Leu	Ser	Ser	Ser	Leu	Asp	Ile	Gln
Asp 625	Ser	Glu	Asp	Glu	Glu	Asp	Gly	Ser	Asn	Ser	Gln	Ala	Phe	Arg	Cys
Val	Pro	Gly	Thr	Val	Val	Arg	Thr	Leu	Met	Glu	Ala	Ile	Ala	Lys	Arg
Leu	Asp	Ala	Cys	Gln	Glu	Gln	Leu	Leu	Glu	Leu	Tyr	Glu	Glu	Asn	Ser

Thr	Asp	Leu	His	Lys	His	Val	Leu	His	Trp	Lys	Cys	Met	Arg	His	Glu	
		675					680					685				
Ser	Val	Leu	Leu	Tyr	Lys	Ala	Lys	Gln	Met	Gly	Leu	Ser	His	Ile	Gly	
		690				695					700					
Met	Gln	Val	Val	Pro	Pro	Leu	Lys	Val	Ser	Glu	Ala	Lys	Gly	His	Asn	
705					710					715					720	
Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	Ser	Leu	Leu	Arg	Thr	Glu	Tyr	
			725						730					735		
Ser	Met	Glu	Pro	Trp	Thr	Leu	Gln	Glu	Thr	Ser	Tyr	Glu	Met	Trp	Gln	
			740					745						750		
Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	Arg	Gly	Lys	Thr	Val	Glu	Val	
		755					760						765			
Lys	Phe	Asp	Gly	Cys	Ala	Asn	Asn	Thr	Met	Asp	Tyr	Val	Val	Trp	Thr	
	770					775					780					
Asp	Val	Tyr	Val	Gln	Asp	Asn	Asp	Thr	Trp	Val	Lys	Val	His	Ser	Met	
785					790					795					800	
Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr	Cys	Gly	Gln	Phe	Lys	Thr	Tyr	
				805					810					815		
Tyr	Val	Asn	Phe	Val	Lys	Glu	Ala	Glu	Lys	Tyr	Gly	Ser	Thr	Lys	His	
		820						825					830			
Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val	Ile	Cys	Ser	Pro	Ala	Ser	Val	
		835					840						845			
Ser	Ser	Thr	Thr	Gln	Glu	Val	Ser	Ile	Pro	Glu	Ser	Thr	Thr	Tyr	Thr	
		850				855						860				
Pro	Ala	Gln	Thr	Ser	Thr	Leu	Val	Ser	Ser	Ser	Thr	Lys	Glu	Asp	Ala	
865					870					875					880	
Val	Gln	Thr	Pro	Pro	Arg	Lys	Arg	Ala	Arg	Gly	Val	Gln	Gln	Ser	Pro	
				885					890					895		
Cys	Asn	Ala	Leu	Cys	Val	Ala	His	Ile	Gly	Pro	Val	Asp	Ser	Gly	Asn	
		900						905						910		
His	Asn	Leu	Ile	Thr	Asn	Asn	His	Asp	Gln	His	Gln	Arg	Arg	Asn	Asn	
		915					920					925				
Ser	Asn	Ser	Ser	Ala	Thr	Pro	Ile	Val	Gln	Phe	Gln	Gly	Glu	Ser	Asn	
		930				935					940					
Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn	Asp	Arg	His	Arg	His	Leu	
945					950					955					960	
Phe	Asp	Leu	Ile	Ser	Ser	Thr	Trp	His	Trp	Ala	Ser	Ser	Lys	Ala	Pro	
				965					970					975		
His	Lys	His	Ala	Ile	Val	Thr	Val	Thr	Tyr	Asp	Ser	Glu	Glu	Gln	Arg	
			980					985					990			
Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile	Pro	Pro	Thr	Ile	Ser	His	Lys	
		995					1000					1005				
Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu	Met	Glu	Ala	Ile	Ala	Lys	Arg	
						1015					1020					
Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu	Glu	Leu	Tyr	Glu	Glu	Asn	Ser	
1025					1030					1035					1040	
Ile	Asp	Ile	His	Lys	His	Ile	Met	His	Trp	Lys	Cys	Ile	Arg	Leu	Glu	
				1045					1050					1055		
Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln	Met	Gly	Leu	Ser	His	Ile	Gly	
				1060				1065					1070			
Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val	Ser	Glu	Thr	Lys	Gly	His	Asn	
		1075					1080					1085				
Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	Ser	Leu	Ala	Lys	Thr	Gln	Tyr	
		1090				1095					1100					
Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp	Thr	Ser	Tyr	Glu	Met	Trp	Leu	
1105					1110					1115					1120	
Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	Gln	Gly	Asn	Thr	Val	Glu	Val	
				1125					1130					1135		
Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val	Met	Glu	Tyr	Val	Val	Trp	Thr	

1140	1145	1150
His Ile Tyr Leu Gln Asp Asn Asp Ser Trp Val Lys Val Thr Ser Ser		
1155	1160	1165
Val Asp Ala Lys Gly Ile Tyr Tyr Thr Cys Gly Gln Phe Lys Thr Tyr		
1170	1175	1180
Tyr Val Asn Phe Asn Lys Glu Ala Gln Lys Tyr Gly Ser Thr Asn His		
1185	1190	1195
Trp Glu Val Cys Tyr Gly Ser Thr Val Ile Cys Ser Pro Ala Ser Val		
1205	1210	1215
Ser Ser Thr Val Arg Glu Val Ser Ile Ala Glu Pro Thr Thr Tyr Thr		
1220	1225	1230
Pro Ala Gln Thr Thr Ala Pro Thr Val Ser Ala Cys Thr Thr Glu Asp		
1235	1240	1245
Gly Val Ser Ala Pro Pro Arg Lys Arg Ala Arg Gly Pro Ser Thr Asn		
1250	1255	1260
Asn Thr Leu Cys Val Ala Asn Ile Arg Ser Val Asp Ser Thr Ile Asn		
1265	1270	1275
Asn Ile Val Thr Asp Asn Tyr Asn Lys His Gln Arg Arg Asn Asn Cys		
1285	1290	1295
His Ser Ala Ala Thr Pro Ile Val Gln Leu Gln Gly Asp Ser Asn Cys		
1300	1305	1310
Leu Lys Cys Phe Arg Tyr Arg Leu Asn Asp Lys Tyr Lys His Leu Phe		
1315	1320	1325
Glu Leu Ala Ser Ser Thr Trp His Trp Ala Ser Pro Glu Ala Pro His		
1330	1335	1340
Lys Asn Ala Ile Val Thr Leu Thr Tyr Ser Ser Glu Glu Gln Arg Gln		
1345	1350	1355
Gln Phe Leu Asn Ser Val Lys Ile Pro Pro Thr Ile Arg His Lys Val		
1365	1370	1375
Gly Phe Met Ser Leu His Leu Leu		
1380		

<210> 19  
 <211> 4155  
 <212> DNA  
 <213> HPV

<400> 19

atggaagcta	ttgccaagcg	actggacgcc	tgccaggagc	agctgctgga	gctgtacgag	60
gaaaacagca	cagacctcca	caagcacgtg	ctgcactgga	agtgcattgcg	ccacgagtc	120
gtgctcctgt	acaaggccaa	gcagatgggg	ctgtcccaca	tcgggatgca	ggctgtgccc	180
ccgctgaagg	tgagcgaagc	caagggccac	aacgctatcg	agatgcagat	gcacctggag	240
agcctgctgc	ggaccgaata	cagcatggag	ccctggactc	tccaggagac	gtcctacgaa	300
atgtggcaga	ctcctccgaa	gcgctgtttc	gcaaagcgcg	gcaagacagt	tgaggtgaaa	360
ttcgtatgggt	gcgcaaacia	cacgatggac	tacgtggtgt	ggaccgatgt	ctacgtgcag	420
gacaatgaca	cctgggtgaa	ggtacatagt	atggtggatg	ccaagggcat	ctattacacc	480
tgcgggcagc	tcaagacgta	ctacgtcaac	ttcgtcaagg	aagccgaaaa	gtatggttcc	540
accaagcact	gggaggtgtg	ttacggggagt	actgtgatct	gcagccccgc	ctccgtgtcg	600
tccaaccaccc	aggaagtgcg	cattccggag	agcaccacat	acaccccggc	ccaaacgagc	660
acgctcgtca	gcagcagcac	caaggaggac	gccgtccaga	cgcccccccg	gaagagggcc	720
cgggggggtcc	agcagtcctc	ctgcaatgcc	ctgtgcgttg	ctcacatcgg	ccctgtcgat	780
tctgggaacc	acaatctcat	cacgaacaac	cacgaccagc	accaaaggcg	caacaactct	840
aacagctccg	caactccaat	agtgcagttc	cagggggagt	ccaactgcct	caagtgtttc	900
cgctaccgcc	tcaacgaccg	ccaccgccac	ctgttcgact	tgatcagttc	cacgtggcac	960
tggggccagca	gcaagcgccc	ccacaaacac	gcatcgtga	cggtgacct	cgactccgag	1020
gagcagagggc	agcagttcct	ggacgtcgtg	aagattcctc	cgacaatcag	ccacaagctt	1080
ggcttcatgt	ccctgcacct	gctgatggca	gacgattccg	gtactgagaa	cgaaggttct	1140
ggttggtaccg	ggttggttcat	ggttgaagca	atcgttcagc	atccgactgg	taccagatc	1200

tccgatgacg	aagacgaaga	agttgaagat	tctgggttacg	acatgggttga	cttcacatgat	1260
gactccaaca	tcactcataa	ctctctggaa	gcacaggctc	tgtttaaccg	ccaggaagct	1320
gatacccatt	acgtactgt	tcaggacctg	ggaggcaaat	atctgggctc	tccgtacgtt	1380
tccccgatca	acactatcgc	agaagcagtt	gagtctgaaa	tctccccgcg	cctggacgct	1440
atcaaactga	ctcgtcagcc	gaagaaggtt	aaacgtcgtc	tgttccagac	tcgtgaactg	1500
accgactccg	gttacggtta	tagcgaagtt	gaggctggca	ccggcaccga	ggttgaaaaa	1560
cacggtgtac	cggaaaacgg	cggcgacggg	caggaaaagg	acaccggccg	cgacatcgag	1620
ggtgaggaac	acaccgaagc	tgaagctccg	actaactctg	ttcgtgaaca	cgcaggtact	1680
gcgggtatcc	tggaaactgct	gaaatgcaaa	gacctgcgcg	cggctctgct	gggcaaattc	1740
aaagaatgct	ctggcctgtc	tttcattgac	ctgatccgtc	cgtttaagtc	tgacaaaact	1800
acctgtctgg	actgggttgt	agcaggcttc	ggcatccacc	actctatctc	tgaagcatte	1860
cagaaactga	tcgagccgct	gtctctgtac	gcgcacatcc	agtggctgac	taacgcttgg	1920
ggtatggttc	tgctgggtact	gctgcgcttt	aaagtaaaca	aatctcgttc	cactgtttgt	1980
cgtactctgg	ctaccctgct	gaacatcccg	gagaaccaga	tgctgatcga	accgccgaaa	2040
atccagtctg	gtgtagctgc	actgtactgg	tttcgtactg	gcactctctaa	cgctagcact	2100
gttatcgggtg	aagcaccgga	atggatcact	cgtcagaccg	ttatcgaaca	cggctctggca	2160
gattctcagt	tcaaactgac	tgaatgggtt	cagtgggcat	acgacaacga	catctgcgag	2220
gaatctgaaa	ttgcgttcga	atacgtctag	cgtggcgact	tcgactccaa	cgctcgtgct	2280
ttcctgaaca	gcaacatgca	ggctaaatac	gtaaaagact	gcgctaccat	gtgcgctcac	2340
tacaaacacg	cggaaatgcg	taaaatgtct	atcaaacagt	ggatcaagca	ccgcggttct	2400
aaaatcgaag	taccgggtaa	ctggaaacgg	atcgttcagt	tcctgcgcca	tcagaacatc	2460
gaattcatcc	cgttctctgac	caaattcaag	ctgtggctgc	acggtacccc	gaaaaaaaaa	2520
tgcatcgcta	tcgtaggtcc	accggacact	gacaagtctt	acttctgtat	gtccctgac	2580
tctttctctg	gcggcactgt	aatctctcac	gttaactctt	cctcccattt	ctggctgcag	2640

ccactggtag	acgcgaaagt	agctctgctg	gacgacgcga	cccagccgtg	ctggatctac	2700
atggatactt	acatgcgcaa	cctgctggac	ggtaaccgga	tgtctatcga	ccgtaaacac	2760
aaagcgctga	ctctgatcaa	gtgcccgccg	ctgctggtaa	cttctaacat	cgacatcacc	2820
aaggaagata	aatacaagta	cctgcatacc	cgtgttacta	cctttacttt	ccgaaccg	2880
ttcccgtttg	atcgtaacgg	taacgctgtt	tacgaactgt	ccaacactaa	ctggaaatgc	2940
ttcttcgagc	gtctgtcttc	ctccctggac	atccaggact	ctgaagatga	agaagatggg	3000
tctaactctc	aggctttccg	ttgtgttccg	ggtagctgtg	ttcgtactct	gatggaagcc	3060
atcgcgaa	ggctcgacgc	ctgccaggac	cagctgctcg	agctgtacga	ggagaacagc	3120
attgacatcc	ataagcacat	catgcactgg	aagtgcattc	gcctggagag	cgtgctgttg	3180
cacaaggcca	agcagatggg	cctgtcccac	ataggccttc	aggtgggtccc	ccctctgacc	3240
gtgtcagaga	caaagggcca	taacgcaatc	gagatgcaga	tgcacctcga	gtcgtggcg	3300
aaaacacagt	acggcggtga	gccatggacc	ctgcaggaca	cctcgtacga	aatgtggctg	3360
accccaccta	agcgatgctt	cgccaaacag	ggcaacacag	tggaggtgaa	gttcgacggc	3420
tgtgaggata	acgttatgga	gtatgtcgtg	tggacgcaca	tctatctgca	ggacaacgac	3480
agttgggtga	aggtgaccag	ctccgtggac	gcgaagggca	tctactatac	ctgtgggcag	3540
tttaaaacct	actatgtgaa	cttcaacaaa	gaggcccaaa	agtatggctc	caccaaccac	3600
tgggaggtct	gctatgggag	cacggtgatt	tgctctcccg	ccagcgtgtc	tagcactgtg	3660
cgcgaggtga	gcattgccga	gccgaccacg	tacaccctcg	cccagacgac	cgctccgacc	3720
gtgtctgctt	gtactaccga	ggacggcggtg	agcgctccac	ccaggaagcg	tgcgaggggc	3780
ccaagcacca	acaacaccct	ctgtgtggcg	aacattcgca	gcgtcgacag	taccatcaat	3840
aacatcgtga	cggataacta	taacaagcac	cagaggcgta	acaactgtca	ctctgccgca	3900
acccccatcg	tgcagctcca	gggagacagc	aattgcctta	agtgcctccg	ctatgcctc	3960
aacgacaagt	acaagcacct	ctttgagctc	gcctcgctga	cgtggcactg	ggcctcacc	4020
gaggcacctc	acaagaacgc	catcgctcact	ctcacttact	ccagtgagga	gcagagacag	4080
cagtttctga	acagcgtgaa	gatccccaccg	acgatccgtc	ataaggctcg	cttcattgtca	4140
ctgcatctcc	tgtga					4155

<210> 20  
 <211> 1384  
 <212> PRT  
 <213> HPV

<400> 20  
 Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Glu Gln Leu Leu

1				5					10				15			
Glu	Leu	Tyr	Glu	Glu	Asn	Ser	Thr	Asp	Leu	His	Lys	His	Val	Leu	His	
			20					25					30			
Trp	Lys	Cys	Met	Arg	His	Glu	Ser	Val	Leu	Leu	Tyr	Lys	Ala	Lys	Gln	
		35					40					45				
Met	Gly	Leu	Ser	His	Ile	Gly	Met	Gln	Val	Val	Pro	Pro	Leu	Lys	Val	
	50					55					60					
Ser	Glu	Ala	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	
65					70				75						80	
Ser	Leu	Leu	Arg	Thr	Glu	Tyr	Ser	Met	Glu	Pro	Trp	Thr	Leu	Gln	Glu	
				85					90					95		
Thr	Ser	Tyr	Glu	Met	Trp	Gln	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	
			100					105					110			
Arg	Gly	Lys	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Ala	Asn	Asn	Thr	
		115					120					125				
Met	Asp	Tyr	Val	Val	Trp	Thr	Asp	Val	Tyr	Val	Gln	Asp	Asn	Asp	Thr	
	130					135					140					
Trp	Val	Lys	Val	His	Ser	Met	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr	
145					150					155					160	
Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Val	Lys	Glu	Ala	Glu	
				165				170							175	
Lys	Tyr	Gly	Ser	Thr	Lys	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val	
			180					185					190			
Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Thr	Gln	Glu	Val	Ser	Ile	
	195						200					205				
Pro	Glu	Ser	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Ser	Thr	Leu	Val	Ser	
	210					215					220					
Ser	Ser	Thr	Lys	Glu	Asp	Ala	Val	Gln	Thr	Pro	Pro	Arg	Lys	Arg	Ala	
225					230					235					240	
Arg	Gly	Val	Gln	Gln	Ser	Pro	Cys	Asn	Ala	Leu	Cys	Val	Ala	His	Ile	
				245				250							255	
Gly	Pro	Val	Asp	Ser	Gly	Asn	His	Asn	Leu	Ile	Thr	Asn	Asn	His	Asp	
			260					265					270			
Gln	His	Gln	Arg	Arg	Asn	Asn	Ser	Asn	Ser	Ser	Ala	Thr	Pro	Ile	Val	
	275						280					285				
Gln	Phe	Gln	Gly	Glu	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	
	290					295				300						
Asn	Asp	Arg	His	Arg	His	Leu	Phe	Asp	Leu	Ile	Ser	Ser	Thr	Trp	His	
305					310					315					320	
Trp	Ala	Ser	Ser	Lys	Ala	Pro	His	Lys	His	Ala	Ile	Val	Thr	Val	Thr	
				325				330							335	
Tyr	Asp	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile	
			340					345					350			
Pro	Pro	Thr	Ile	Ser	His	Lys	Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu	
		355					360				365					
Met	Ala	Asp	Asp	Ser	Gly	Thr	Glu	Asn	Glu	Gly	Ser	Gly	Cys	Thr	Gly	
	370					375				380						
Trp	Phe	Met	Val	Glu	Ala	Ile	Val	Gln	His	Pro	Thr	Gly	Thr	Gln	Ile	
385					390				395						400	
Ser	Asp	Asp	Glu	Asp	Glu	Glu	Val	Glu	Asp	Ser	Gly	Tyr	Asp	Met	Val	
				405				410						415		
Asp	Phe	Ile	Asp	Asp	Ser	Asn	Ile	Thr	His	Asn	Ser	Leu	Glu	Ala	Gln	
			420					425					430			
Ala	Leu	Phe	Asn	Arg	Gln	Glu	Ala	Asp	Thr	His	Tyr	Ala	Thr	Val	Gln	
		435					440					445				
Asp	Leu	Gly	Gly	Lys	Tyr	Leu	Gly	Ser	Pro	Tyr	Val	Ser	Pro	Ile	Asn	
	450					455				460						
Thr	Ile	Ala	Glu	Ala	Val	Glu	Ser	Glu	Ile	Ser	Pro	Arg	Leu	Asp	Ala	
465					470				475						480	

Ile	Lys	Leu	Thr	Arg	Gln	Pro	Lys	Lys	Val	Lys	Arg	Arg	Leu	Phe	Gln
				485					490					495	
Thr	Arg	Glu	Leu	Thr	Asp	Ser	Gly	Tyr	Gly	Tyr	Ser	Glu	Val	Glu	Ala
			500					505					510		
Gly	Thr	Gly	Thr	Gln	Val	Glu	Lys	His	Gly	Val	Pro	Glu	Asn	Gly	Gly
		515					520					525			
Asp	Gly	Gln	Glu	Lys	Asp	Thr	Gly	Arg	Asp	Ile	Glu	Gly	Glu	Glu	His
	530					535				540					
Thr	Glu	Ala	Glu	Ala	Pro	Thr	Asn	Ser	Val	Arg	Glu	His	Ala	Gly	Thr
545					550					555					560
Ala	Gly	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Lys	Asp	Leu	Arg	Ala	Ala	Leu
			565					570						575	
Leu	Gly	Lys	Phe	Lys	Glu	Cys	Phe	Gly	Leu	Ser	Phe	Ile	Asp	Leu	Ile
			580					585					590		
Arg	Pro	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Leu	Asp	Trp	Val	Val	Ala
		595					600					605			
Gly	Phe	Gly	Ile	His	His	Ser	Ile	Ser	Glu	Ala	Phe	Gln	Lys	Leu	Ile
	610					615					620				
Glu	Pro	Leu	Ser	Leu	Tyr	Ala	His	Ile	Gln	Trp	Leu	Thr	Asn	Ala	Trp
625					630					635					640
Gly	Met	Val	Leu	Leu	Val	Leu	Leu	Arg	Phe	Lys	Val	Asn	Lys	Ser	Arg
			645						650					655	
Ser	Thr	Val	Ala	Arg	Thr	Leu	Ala	Thr	Leu	Leu	Asn	Ile	Pro	Glu	Asn
			660					665					670		
Gln	Met	Leu	Ile	Glu	Pro	Pro	Lys	Ile	Gln	Ser	Gly	Val	Ala	Ala	Leu
		675					680					685			
Tyr	Trp	Phe	Arg	Thr	Gly	Ile	Ser	Asn	Ala	Ser	Thr	Val	Ile	Gly	Glu
	690					695					700				
Ala	Pro	Glu	Trp	Ile	Thr	Arg	Gln	Thr	Val	Ile	Glu	His	Gly	Leu	Ala
705					710					715					720
Asp	Ser	Gln	Phe	Lys	Leu	Thr	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp	Asn
			725						730					735	
Asp	Ile	Cys	Glu	Glu	Ser	Glu	Ile	Ala	Phe	Glu	Tyr	Ala	Gln	Arg	Gly
		740						745					750		
Asp	Phe	Asp	Ser	Asn	Ala	Arg	Ala	Phe	Leu	Asn	Ser	Asn	Met	Gln	Ala
	755						760					765			
Lys	Tyr	Val	Lys	Asp	Cys	Ala	Thr	Met	Cys	Arg	His	Tyr	Lys	His	Ala
	770					775					780				
Glu	Met	Arg	Lys	Met	Ser	Ile	Lys	Gln	Trp	Ile	Lys	His	Arg	Gly	Ser
785					790					795					800
Lys	Ile	Glu	Gly	Thr	Gly	Asn	Trp	Lys	Pro	Ile	Val	Gln	Phe	Leu	Arg
			805						810					815	
His	Gln	Asn	Ile	Glu	Phe	Ile	Pro	Phe	Leu	Thr	Lys	Phe	Lys	Leu	Trp
		820						825					830		
Leu	His	Gly	Thr	Pro	Lys	Lys	Asn	Cys	Ile	Ala	Ile	Val	Gly	Pro	Pro
		835					840					845			
Asp	Thr	Asp	Lys	Ser	Tyr	Phe	Cys	Met	Ser	Leu	Ile	Ser	Phe	Leu	Gly
	850					855					860				
Gly	Thr	Val	Ile	Ser	His	Val	Asn	Ser	Ser	Ser	His	Phe	Trp	Leu	Gln
865					870					875					880
Pro	Leu	Val	Asp	Ala	Lys	Val	Ala	Leu	Leu	Asp	Asp	Ala	Thr	Gln	Pro
			885						890					895	
Cys	Trp	Ile	Tyr	Met	Asp	Thr	Tyr	Met	Arg	Asn	Leu	Leu	Asp	Gly	Asn
		900						905					910		
Pro	Met	Ser	Ile	Asp	Arg	Lys	His	Lys	Ala	Leu	Thr	Leu	Ile	Lys	Cys
		915					920					925			
Pro	Pro	Leu	Leu	Val	Thr	Ser	Asn	Ile	Asp	Ile	Thr	Lys	Glu	Asp	Lys
	930					935					940				
Tyr	Lys	Tyr	Leu	His	Thr	Arg	Val	Thr	Thr	Phe	Thr	Phe	Pro	Asn	Pro

945					950					955					960
Phe	Pro	Phe	Asp	Arg	Asn	Gly	Asn	Ala	Val	Tyr	Glu	Leu	Ser	Asn	Thr
				965						970				975	
Asn	Trp	Lys	Cys	Phe	Phe	Glu	Arg	Leu	Ser	Ser	Ser	Leu	Asp	Ile	Gln
			980					985					990		
Asp	Ser	Glu	Asp	Glu	Glu	Asp	Gly	Ser	Asn	Ser	Gln	Ala	Phe	Arg	Cys
		995					1000					1005			
Val	Pro	Gly	Thr	Val	Val	Arg	Thr	Leu	Met	Glu	Ala	Ile	Ala	Lys	Arg
		1010					1015					1020			
Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu	Glu	Leu	Tyr	Glu	Glu	Asn	Ser
1025						1030					1035				1040
Ile	Asp	Ile	His	Lys	His	Ile	Met	His	Trp	Lys	Cys	Ile	Arg	Leu	Glu
				1045						1050				1055	
Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln	Met	Gly	Leu	Ser	His	Ile	Gly
			1060					1065					1070		
Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val	Ser	Glu	Thr	Lys	Gly	His	Asn
		1075					1080					1085			
Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu	Ser	Leu	Ala	Lys	Thr	Gln	Tyr
		1090					1095					1100			
Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp	Thr	Ser	Tyr	Glu	Met	Trp	Leu
1105						1110					1115				1120
Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys	Gln	Gly	Asn	Thr	Val	Glu	Val
				1125					1130					1135	
Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val	Met	Glu	Tyr	Val	Val	Trp	Thr
			1140					1145					1150		
His	Ile	Tyr	Leu	Gln	Asp	Asn	Asp	Ser	Trp	Val	Lys	Val	Thr	Ser	Ser
		1155					1160					1165			
Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr	Cys	Gly	Gln	Phe	Lys	Thr	Tyr
		1170				1175					1180				
Tyr	Val	Asn	Phe	Asn	Lys	Glu	Ala	Gln	Lys	Tyr	Gly	Ser	Thr	Asn	His
1185					1190					1195					1200
Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val	Ile	Cys	Ser	Pro	Ala	Ser	Val
			1205					1210					1215		
Ser	Ser	Thr	Val	Arg	Glu	Val	Ser	Ile	Ala	Glu	Pro	Thr	Thr	Tyr	Thr
			1220					1225					1230		
Pro	Ala	Gln	Thr	Thr	Ala	Pro	Thr	Val	Ser	Ala	Cys	Thr	Thr	Glu	Asp
		1235					1240					1245			
Gly	Val	Ser	Ala	Pro	Pro	Arg	Lys	Arg	Ala	Arg	Gly	Pro	Ser	Thr	Asn
		1250				1255					1260				
Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg	Ser	Val	Asp	Ser	Thr	Ile	Asn
1265					1270					1275					1280
Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys	His	Gln	Arg	Arg	Asn	Asn	Cys
			1285					1290					1295		
His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln	Leu	Gln	Gly	Asp	Ser	Asn	Cys
		1300					1305					1310			
Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn	Asp	Lys	Tyr	Lys	His	Leu	Phe
		1315					1320					1325			
Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp	Ala	Ser	Pro	Glu	Ala	Pro	His
		1330				1335					1340				
Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr	Ser	Ser	Glu	Glu	Gln	Arg	Gln
1345					1350					1355					1360
Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro	Pro	Thr	Ile	Arg	His	Lys	Val
			1365					1370					1375		
Gly	Phe	Met	Ser	Leu	His	Leu	Leu								
			1380												

<210> 21  
<211> 4155



<212> DNA

<213> HPV

<400> 21

atggaagcta	ttgccaagcg	actggacgcc	tgccaggagc	agctgctgga	gctgtacgag	60
gaaaacagca	cagacctcca	caagcacgtg	ctgcaactgga	agtgcattgcg	ccacgagtc	120
gtgctcctgt	acaaggccaa	gcagatgggg	ctgtcccaca	tcgggatgca	ggctgtgccc	180
ccgctgaagg	tgagcgaagc	caagggccac	aacgctatcg	agatgcagat	gcacctggag	240
agcctgctgc	ggaccgaata	cagcatggag	ccctggactc	tccaggagac	gtcctacgaa	300
atgtggcaga	ctcctccgaa	gcgctgtttc	gcaaagcgcg	gcaagacagt	tgagggtgaa	360
ttcgatgggt	gcgcaaacaa	cacgatggac	tacgtgggtg	ggaccgatgt	ctacgtgcag	420
gacaatgaca	cctgggtgaa	ggtacatagt	atgggtggatg	ccaagggcat	ctattacacc	480
tgccgggcagt	tcaagacgta	ctacgtcaac	ttcgtcaagg	aagccgaaaa	gtatggttcc	540
accaagcact	gggaggtgtg	ttacgggagt	actgtgatct	gcagccccgc	ctccgtgtcg	600
tccaccaccc	aggaagtgag	cattccggag	agcaccacat	acacccccgc	ccaaacgagc	660
acgctcgtca	gcagcagcac	caaggaggac	gccgtccaga	cgcccccccg	gaagagggcc	720
cgggggggtcc	agcagtctcc	ctgcaatgcc	ctgtgcgttg	ctcacatcgg	ccctgtcgat	780
tctgggaacc	acaatctcat	cacgaacaac	cacgaccagc	accaaaggcg	caacaactct	840
aacagctccg	caactccaat	agtgcagttc	cagggggagt	ccaactgcct	caagtgtttc	900
cgctaccgcc	tcaacgaccg	ccaccgccac	ctgttcgact	tgatcagttc	cacgtggcac	960
tgggccagca	gcaaggcgcc	ccacaaacac	gctatcgtga	cgggtgacct	cgactccgag	1020
gagcagaggc	agcagttcct	ggacgtcgtg	aagattcctc	cgacaatcag	ccacaagctt	1080
ggcttcatgt	ccctgcacct	gctgatggaa	gccatcgoga	agaggctcga	cgcttgccag	1140
gaccagctgc	tcgagctgta	cgaggagaac	agcattgaca	tccataagca	catcatgcac	1200
tggaagtgca	ttcgcttgga	gagcgtgctg	ttgcacaagg	ccaagcagat	gggcctgtcc	1260
cacataggcc	ttcaggtggt	ccccctctg	accgtgtcag	agacaaaagg	ccataacgca	1320
atcgagatgc	agatgcacct	cgagtcgctg	gcgaaaacac	agtacggcgt	ggagccatgg	1380
accctgcagg	acacctcgta	cgaaatgtgg	ctgacccccc	ctaagcgatg	cttcgccaaa	1440
cagggcaaca	cagtggaagt	gaagtctcag	ggctgtgagg	ataacgttat	ggagtatgtc	1500
gtgtggacgc	acatctatct	gcaggacaac	gacagttggg	tgaaggtgac	cagctccgtg	1560
gacgcgaagg	gcattctact	tacctgtggg	cagtttataa	cctactatgt	gaacttcaac	1620
aaagaggccc	aaaagtatgg	ctccaccaac	cactgggagg	tctgctatgg	gagcacggtg	1680
atttgctctc	ccgccagcgt	gtctagcact	gtgcgcgagg	tgagcattgc	cgagccgacc	1740
acgtacaccc	ctgcccagac	gaccgctccg	accgtgtctg	cttggtactac	cgaggacggc	1800
gtgagcgctc	cacccaggaa	gcgtgcgagg	ggcccaagca	ccaacaacac	cctctgtgtg	1860
gcgaacattc	gcagcgtcga	cagtaccatc	aataacatcg	tgacggataa	ctataacaag	1920
caccagaggc	gtaacaactg	tactcttgcc	gcaaccccc	tcgtgcagct	ccaggagagc	1980
agcaattgcc	ttaagtgtct	ccgctatcgc	ctcaacgaca	agtacaagca	cctctttgag	2040
ctcgctcgtg	cgacgtggca	ctgggcctca	cccgaggcac	ctcacaagaa	cgccatcgtc	2100
actctcactt	actccagtga	ggagcagaga	cagcagtttc	tgaacagcgt	gaagatccca	2160
ccgacgatcc	gtcataaggt	cggcttcatg	tactgcctc	tcctgatggc	agacgattcc	2220
ggtactgaga	acgaagggtc	tggttggtacc	gggttggttca	tggttgaagc	aatcggttcag	2280
catccgactg	gtaccagatg	ctccgatgac	gaagacgaag	aagttgaaga	ttctgggttac	2340
gacatgggtg	acttcatcga	tgactccaac	atcactcata	actctctgga	agcacaggct	2400
ctgtttaacc	gccaggaagc	tgatacccat	tacgtactgt	ttcaggacct	gggaggcaaa	2460
tatctgggct	ctccgtacgt	ttccccgatc	aacactatcg	cagaagcagt	tgagtctgaa	2520
atctccccgc	gcttggaacg	tatcaaaactg	actcgtcagc	cgaagaaggt	taaacgtcgt	2580
ctgttccaga	ctcgtgaact	gaccgactcc	ggttacgggt	atagcgaagt	tgaggctggc	2640
accggcaccc	agggtgaaaa	acacgggtgta	ccggaaaaacg	gcggcgacgg	tcaggaaaag	2700
gacaccggcc	gcgacatcga	gggtgaggaa	cacaccgaag	ctgaagctcc	gactaactct	2760
gttcgtgaac	acgcagggtac	tgccgggtatc	ctggaactgc	tgaaatgcaa	agacctgcgc	2820
gcggctctgc	tgggcaaatt	caaagaatgc	ttcggcctgt	ctttcattga	cctgatccgt	2880
ccgtttaagt	ctgacaaaac	tacctgtctg	gactgggttg	tagcaggctt	cggcatccac	2940
cactctatct	ctgaagcatt	ccagaaaactg	atcgagccgc	tgtctctgta	cgcgcacatc	3000
cagtggctga	ctaacgcttg	gggtatgggt	ctgctgggtac	tgctgcgctt	taaagtaaac	3060
aaatctcgtt	ccactgttgc	tcgtactctg	gctaccctgc	tgaacatccc	ggagaaccag	3120
atgctgatcg	aaccgccgaa	aatccagtct	ggtgtagctg	cactgtactg	gtttcgtact	3180
ggcatctcta	acgctagcac	tgttatcggg	gaagcaccgg	aatggatcac	tcgtcagacc	3240
gttatcgaac	acggtctggc	agattctcag	ttcaaactga	ctgaaatggg	tcagtgggca	3300

```

tacgacaacg acatctgcga ggaatctgaa attgcgttcg aatagctca gcggtggcgac 3360
ttcgactcca acgctcgtgc tttcctgaac agcaacatgc aggctaaata cgtaaaagac 3420
tgcgctacca tgtgccgtca ctacaaacac gcggaaatgc gtaaaatgtc tatcaaacag 3480
tggtatcaagc accgcggttc taaaatcgaa ggtaccggta actggaaacc gatcgttcag 3540
ttcctgcgcc atcagaacat cgaattcatc ccgttcctga ccaaattcaa gctgtggctg 3600
cacggtaccc cgaaaaaaaa ctgcatcgct atcgtagggtc caccggacac tgacaagtct 3660
tactttctgta tgtccctgat ctctttcctg ggccggcactg taatctctca cgtaactct 3720
tcctcccatt tctggctgca gccactggta gacgcgaaag tagctctgct ggacgacgcg 3780
acccagccgt gctggatcta catggatact tacatgcgca acctgctgga cggtaaccgc 3840
atgtctatcg accgtaaaca caaagcgtg actctgatca agtgcccgcc gctgctggta 3900
acttctaaca tcgacatcac caaggaagat aaatacaagt acctgcatac ccgtgttact 3960
acctttactt tcccgaaccc gttcccgttt gatcgtaacg gtaacgctgt ttacgaactg 4020
tccaacacta actggaaatg cttcttcgag cgtctgtctt cctccctgga catccaggac 4080
tctgaagatg aagaagatgg ttctaactct caggctttcc gttgtgttcc ggggtactgtt 4140
gttcgtactc tgtga                                     4155

```

<210> 22

<211> 1384

<212> PRT

<213> HPV

<400> 22

```

Met Glu Ala Ile Ala Lys Arg Leu Asp Ala Cys Gln Glu Gln Leu Leu
 1          5          10          15
Glu Leu Tyr Glu Glu Asn Ser Thr Asp Leu His Lys His Val Leu His
 20          25          30
Trp Lys Cys Met Arg His Glu Ser Val Leu Leu Tyr Lys Ala Lys Gln
 35          40          45
Met Gly Leu Ser His Ile Gly Met Gln Val Val Pro Pro Leu Lys Val
 50          55          60
Ser Glu Ala Lys Gly His Asn Ala Ile Glu Met Gln Met His Leu Glu
 65          70          75          80
Ser Leu Leu Arg Thr Glu Tyr Ser Met Glu Pro Trp Thr Leu Gln Glu
 85          90          95
Thr Ser Tyr Glu Met Trp Gln Thr Pro Pro Lys Arg Cys Phe Ala Lys
100          105          110
Arg Gly Lys Thr Val Glu Val Lys Phe Asp Gly Cys Ala Asn Asn Thr
115          120          125
Met Asp Tyr Val Val Trp Thr Asp Val Tyr Val Gln Asp Asn Asp Thr
130          135          140
Trp Val Lys Val His Ser Met Val Asp Ala Lys Gly Ile Tyr Tyr Thr
145          150          155          160
Cys Gly Gln Phe Lys Thr Tyr Tyr Val Asn Phe Val Lys Glu Ala Glu
165          170          175
Lys Tyr Gly Ser Thr Lys His Trp Glu Val Cys Tyr Gly Ser Thr Val
180          185          190
Ile Cys Ser Pro Ala Ser Val Ser Ser Thr Thr Gln Glu Val Ser Ile
195          200          205
Pro Glu Ser Thr Thr Tyr Thr Pro Ala Gln Thr Ser Thr Leu Val Ser
210          215          220
Ser Ser Thr Lys Glu Asp Ala Val Gln Thr Pro Pro Arg Lys Arg Ala
225          230          235          240
Arg Gly Val Gln Gln Ser Pro Cys Asn Ala Leu Cys Val Ala His Ile
245          250          255
Gly Pro Val Asp Ser Gly Asn His Asn Leu Ile Thr Asn Asn His Asp
260          265          270
Gln His Gln Arg Arg Asn Asn Ser Asn Ser Ser Ala Thr Pro Ile Val
275          280          285
Gln Phe Gln Gly Glu Ser Asn Cys Leu Lys Cys Phe Arg Tyr Arg Leu

```

290	Asn	Asp	Arg	His	Arg	His	Leu	Phe	Asp	Leu	Ile	Ser	Ser	Thr	Trp	His
305	Trp	Ala	Ser	Ser	Lys	Ala	Pro	His	Lys	His	Ala	Ile	Val	Thr	Val	Thr
					325					330						335
	Tyr	Asp	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp	Val	Val	Lys	Ile
				340					345						350	
	Pro	Pro	Thr	Ile	Ser	His	Lys	Leu	Gly	Phe	Met	Ser	Leu	His	Leu	Leu
			355					360					365			
	Met	Glu	Ala	Ile	Ala	Lys	Arg	Leu	Asp	Ala	Cys	Gln	Asp	Gln	Leu	Leu
		370					375					380				
	Glu	Leu	Tyr	Glu	Glu	Asn	Ser	Ile	Asp	Ile	His	Lys	His	Ile	Met	His
385						390					395					400
	Trp	Lys	Cys	Ile	Arg	Leu	Glu	Ser	Val	Leu	Leu	His	Lys	Ala	Lys	Gln
				405						410						415
	Met	Gly	Leu	Ser	His	Ile	Gly	Leu	Gln	Val	Val	Pro	Pro	Leu	Thr	Val
				420					425						430	
	Ser	Glu	Thr	Lys	Gly	His	Asn	Ala	Ile	Glu	Met	Gln	Met	His	Leu	Glu
			435					440					445			
	Ser	Leu	Ala	Lys	Thr	Gln	Tyr	Gly	Val	Glu	Pro	Trp	Thr	Leu	Gln	Asp
		450					455					460				
	Thr	Ser	Tyr	Glu	Met	Trp	Leu	Thr	Pro	Pro	Lys	Arg	Cys	Phe	Ala	Lys
465						470					475					480
	Gln	Gly	Asn	Thr	Val	Glu	Val	Lys	Phe	Asp	Gly	Cys	Glu	Asp	Asn	Val
				485						490						495
	Met	Glu	Tyr	Val	Val	Trp	Thr	His	Ile	Tyr	Leu	Gln	Asp	Asn	Asp	Ser
			500						505						510	
	Trp	Val	Lys	Val	Thr	Ser	Ser	Val	Asp	Ala	Lys	Gly	Ile	Tyr	Tyr	Thr
			515					520					525			
	Cys	Gly	Gln	Phe	Lys	Thr	Tyr	Tyr	Val	Asn	Phe	Asn	Lys	Glu	Ala	Gln
		530					535					540				
	Lys	Tyr	Gly	Ser	Thr	Asn	His	Trp	Glu	Val	Cys	Tyr	Gly	Ser	Thr	Val
545						550					555					560
	Ile	Cys	Ser	Pro	Ala	Ser	Val	Ser	Ser	Thr	Val	Arg	Glu	Val	Ser	Ile
				565						570						575
	Ala	Glu	Pro	Thr	Thr	Tyr	Thr	Pro	Ala	Gln	Thr	Thr	Ala	Pro	Thr	Val
			580						585						590	
	Ser	Ala	Cys	Thr	Thr	Glu	Asp	Gly	Val	Ser	Ala	Pro	Pro	Arg	Lys	Arg
			595					600					605			
	Ala	Arg	Gly	Pro	Ser	Thr	Asn	Asn	Thr	Leu	Cys	Val	Ala	Asn	Ile	Arg
		610					615					620				
	Ser	Val	Asp	Ser	Thr	Ile	Asn	Asn	Ile	Val	Thr	Asp	Asn	Tyr	Asn	Lys
625						630					635					640
	His	Gln	Arg	Arg	Asn	Asn	Cys	His	Ser	Ala	Ala	Thr	Pro	Ile	Val	Gln
				645						650						655
	Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe	Arg	Tyr	Arg	Leu	Asn
			660						665						670	
	Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser	Ser	Thr	Trp	His	Trp
			675					680					685			
	Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile	Val	Thr	Leu	Thr	Tyr
			690				695					700				
	Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn	Ser	Val	Lys	Ile	Pro
705						710					715					720
	Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser	Leu	His	Leu	Leu	Met
				725						730						735
	Ala	Asp	Asp	Ser	Gly	Thr	Glu	Asn	Glu	Gly	Ser	Gly	Cys	Thr	Gly	Trp
			740						745					750		
	Phe	Met	Val	Glu	Ala	Ile	Val	Gln	His	Pro	Thr	Gly	Thr	Gln	Ile	Ser
			755					760						765		

Asp	Asp	Glu	Asp	Glu	Glu	Val	Glu	Asp	Ser	Gly	Tyr	Asp	Met	Val	Asp
770						775					780				
Phe	Ile	Asp	Asp	Ser	Asn	Ile	Thr	His	Asn	Ser	Leu	Glu	Ala	Gln	Ala
785					790					795					800
Leu	Phe	Asn	Arg	Gln	Glu	Ala	Asp	Thr	His	Tyr	Ala	Thr	Val	Gln	Asp
				805					810					815	
Leu	Gly	Gly	Lys	Tyr	Leu	Gly	Ser	Pro	Tyr	Val	Ser	Pro	Ile	Asn	Thr
			820					825					830		
Ile	Ala	Glu	Ala	Val	Glu	Ser	Glu	Ile	Ser	Pro	Arg	Leu	Asp	Ala	Ile
		835					840					845			
Lys	Leu	Thr	Arg	Gln	Pro	Lys	Lys	Val	Lys	Arg	Arg	Leu	Phe	Gln	Thr
	850					855				860					
Arg	Glu	Leu	Thr	Asp	Ser	Gly	Tyr	Gly	Tyr	Ser	Glu	Val	Glu	Ala	Gly
865				870					875						880
Thr	Gly	Thr	Gln	Val	Glu	Lys	His	Gly	Val	Pro	Glu	Asn	Gly	Gly	Asp
			885					890						895	
Gly	Gln	Glu	Lys	Asp	Thr	Gly	Arg	Asp	Ile	Glu	Gly	Glu	Glu	His	Thr
			900					905					910		
Glu	Ala	Glu	Ala	Pro	Thr	Asn	Ser	Val	Arg	Glu	His	Ala	Gly	Thr	Ala
		915					920					925			
Gly	Ile	Leu	Glu	Leu	Leu	Lys	Cys	Lys	Asp	Leu	Arg	Ala	Ala	Leu	Leu
	930					935				940					
Gly	Lys	Phe	Lys	Glu	Cys	Phe	Gly	Leu	Ser	Phe	Ile	Asp	Leu	Ile	Arg
945				950					955						960
Pro	Phe	Lys	Ser	Asp	Lys	Thr	Thr	Cys	Leu	Asp	Trp	Val	Val	Ala	Gly
			965					970						975	
Phe	Gly	Ile	His	Ser	Ile	Ser	Glu	Ala	Phe	Gln	Lys	Leu	Ile	Glu	
		980					985					990			
Pro	Leu	Ser	Leu	Tyr	Ala	His	Ile	Gln	Trp	Leu	Thr	Asn	Ala	Trp	Gly
		995					1000					1005			
Met	Val	Leu	Leu	Val	Leu	Leu	Arg	Phe	Lys	Val	Asn	Lys	Ser	Arg	Ser
	1010					1015				1020					
Thr	Val	Ala	Arg	Thr	Leu	Ala	Thr	Leu	Leu	Asn	Ile	Pro	Glu	Asn	Gln
1025				1030						1035					1040
Met	Leu	Ile	Glu	Pro	Pro	Lys	Ile	Gln	Ser	Gly	Val	Ala	Ala	Leu	Tyr
			1045					1050						1055	
Trp	Phe	Arg	Thr	Gly	Ile	Ser	Asn	Ala	Ser	Thr	Val	Ile	Gly	Glu	Ala
		1060					1065					1070			
Pro	Glu	Trp	Ile	Thr	Arg	Gln	Thr	Val	Ile	Glu	His	Gly	Leu	Ala	Asp
		1075					1080					1085			
Ser	Gln	Phe	Lys	Leu	Thr	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp	Asn	Asp
	1090				1095					1100					
Ile	Cys	Glu	Glu	Ser	Glu	Ile	Ala	Phe	Glu	Tyr	Ala	Gln	Arg	Gly	Asp
1105				1110					1115						1120
Phe	Asp	Ser	Asn	Ala	Arg	Ala	Phe	Leu	Asn	Ser	Asn	Met	Gln	Ala	Lys
			1125						1130					1135	
Tyr	Val	Lys	Asp	Cys	Ala	Thr	Met	Cys	Arg	His	Tyr	Lys	His	Ala	Glu
		1140					1145					1150			
Met	Arg	Lys	Met	Ser	Ile	Lys	Gln	Trp	Ile	Lys	His	Arg	Gly	Ser	Lys
		1155					1160					1165			
Ile	Glu	Gly	Thr	Gly	Asn	Trp	Lys	Pro	Ile	Val	Gln	Phe	Leu	Arg	His
	1170				1175						1180				
Gln	Asn	Ile	Glu	Phe	Ile	Pro	Phe	Leu	Thr	Lys	Phe	Lys	Leu	Trp	Leu
1185				1190						1195					1200
His	Gly	Thr	Pro	Lys	Lys	Asn	Cys	Ile	Ala	Ile	Val	Gly	Pro	Pro	Asp
			1205					1210						1215	
Thr	Asp	Lys	Ser	Tyr	Phe	Cys	Met	Ser	Leu	Ile	Ser	Phe	Leu	Gly	Gly
		1220					1225					1230			
Thr	Val	Ile	Ser	His	Val	Asn	Ser	Ser	Ser	His	Phe	Trp	Leu	Gln	Pro

1235	1240	1245
Leu Val Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro Cys		
1250	1255	1260
Trp Ile Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn Pro		
1265	1270	1275
Met Ser Ile Asp Arg Lys His Lys Ala Leu Thr Leu Ile Lys Cys Pro		1280
	1285	1290
Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Thr Lys Glu Asp Lys Tyr		1295
	1300	1305
Lys Tyr Leu His Thr Arg Val Thr Thr Phe Thr Phe Pro Asn Pro Phe		1310
	1315	1320
Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asn Thr Asn		1325
	1330	1335
Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Gln Asp		1340
1345	1350	1355
Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys Val		1360
	1365	1370
Pro Gly Thr Val Val Arg Thr Leu		1375
	1380	

<210> 23  
 <211> 23  
 <212> PRT  
 <213> HPV

<400> 23  
 Cys Ser Ser Ser Leu Asp Ile Gln Asp Ser Glu Asp Glu Glu Asp Gly  
 1 5 10 15  
 Ser Asn Ser Gln Ala Phe Arg  
 20

<210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Immunostimulatory oligonucleotide

<400> 24  
 tccatgacgt tcctgacgtt 20

<210> 25  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Immunostimulatory oligonucleotide

<400> 25  
 tctcccagcg tgcgccat 18

<210> 26  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Immunostimulatory oligonucleotide

<400> 26  
accgatgacg tcgccggtga cggcaccacg 30

<210> 27  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Immunostimulatory oligonucleotide

<400> 27  
tcgtcgtttt gtcgttttgt cggt 24

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Immunostimulatory oligonucleotide

<400> 28  
tccatgacgt tcctgatgct 20  
1

1